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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:14:18 1998; MasPar time 50.54 Seconds 935.076 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113 HASGQRCVLLRTWEALAPAT.....PVEDEALGGTAFVQMPAHGL 949

Scoring table: PAM 150 Gap 11

Searched: 165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_incertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 53.273; Variance 101.693; scale 0.524

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
ב :	6954	97.8	1132	4	014746	TELOMERASE REVERSE TRA	0.00e+00
ພ	6948	97.7	1132	4	014783	CATALYTI	
ω	4087	57.5	1122	11	070372	TELOMERASE REVERSE TRA	0.00e+00
4	675	9.5	989	ω	013338	TELOMERASE REVERSE TRA	N
5	672	9.4	988	w	013339	TELOMERASE REVERSE TRA	9.66e-108
σ	432	6.1	1031	u	000939	TELOMERASE SUBUNIT P12	2.78e-58
7	424	6.0	67	11	035432	TELOMERASE CATALYTIC S	1.11e-56
8	314	4.4	884	ω	Q06163	CHROMOSOME XII COSMID	3.84e-35
9	147	2.1	296	14	269118	HYPOTHETICAL PROTEIN (6.53e-06
10	142	2.0	234	4	000600	PAROTID 'O' PROTEIN (F	3.60e-05
11	141	2.0	276	N	Q46612	IS 1222 GENE ORF-A AND	5.04e-05
12	140	2.0	373	N	054226	POLYKETIDE SYNTHASE (F	7.05e-05
13	143	2.0	574	w	036027	WISKOTT-ALDRICH SYNDRO	2.56e-05
14	136	1.9	316	4	Q99076	HOMEOBOX PROTEIN (FRAG	2.67e-04
15	132	1.9	317	11	Q62103	PROLINE RICH PROTEIN P	9.90e-04
16	133	1.9	539	u	002123	SIMILARITY TO COLLAGEN	7.15e-04
17	135	1.9	585	14	041935	HYPOTHETICAL 60.2 KD P	3.71e-04
18	136	1.9	897	11	070495	PLENTY-OF-PROLINES-101	2.67e-04
19	132	1.9	924	14	Q99307	LF3 PROTEIN.	9.90e-04
20	125	1.8	227	11	Q62107	PROLINE-RICH SALIVARY	9.25e-03

45	44	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21
116	115	115	116	115	117	115	124	122	118	123	124	123	118.	118	118	118	118	126	130	128	125	129	131	129
1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.8	1.8	1.8
488	382	297		260			820			494			437	405	322	236		3247	1236	527	503	309		
10	4	4	11	H	ഗ	14	4	10	14	4	10	10	N	N	N	14	σ	14	N	N	4	4	11	14
004528	000599	Q16038	Q07611	Q64306	Q17626	041981	060585	022835	Q85027	Q15220	Q41645	Q42421	052256	068033	Q53180	Q85028	P91497	Q65553	006264	Q53913	043516	Q04118	Q61888	T08580
SEQUENCE OF BAC F20P5	CON1.	PRB1M PROTEIN (FRAGMEN	PROLINE-RICH PROTEOGLY	PROLINE-RICH PROTEIN.	C04G2.8.	HYPOTHETICAL 9.9 KD PR	SER/ARG-RELATED NUCLEA	SF16 ISOLOG.	VIRAL PROTEINASE.	PRPL-2 PROTEIN.	EXTENSIN (FRAGMENT).	CHITINASE PRECURSOR.	FLHF.	EXONUCLEASE SBCD HOMOL	MPIK3030 NODD1 GENE IN	SUBSTRATE OF THE PROTE	CODED FOR BY C. ELEGAN	UL36.	HYPOTHETICAL 131.9 KD	BETA-KETOACYL SYNTHASE	WASP INTERACTING PROTE	SALIVARY PROLINE-RICH	PROLINE RICH PROTEIN.	HOMOLOGUE OF RETROVIRA
1.45e-01	1.96e-01	1.96e-01	1.45e-01	1.96e-01	1.08e-01	1.96e-01	1.26e-02	2.35e-02	7.98e-02	1.73e-02	1.26e-02	1.73e-02	7.98e-02	7.98e-02	7.98e-02	7.98e-02	7.98e-02	6.75e-03	1.89e-03	3.58e-03	9.25e-03	2.60e-03	1.37e-03	2.606-03

ALIGNMENTS

용	δ S	Qy B	Qy Db	Qy Db	Ma Du	SQ	X D	R.F.	R X	8	RP 3	g 8	88	S 5	B	ĮΤ	DΤ	ij;	58	RESULT
241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300	181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240 	121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALEVLVAPSCAVQVCGPPLYQLGA 180 	61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120 	1 MPRAPRCRAVRSILRSHYREVLPLATEVRRLGÞQGWRLVQRGDÞAAFRALVAQCLVCVPW 60 	Query Match 97.8%; Score 6954; DB 4; Length 1132; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 1132 AA; 126995 MW; 2DFBEDF3 CRC32;	EMBL; AF015950; G2330017; RNA-DIRECTED DNA POLYMERASE.	LINGNER J., HARLEY C.B., CECH T.R.; SCIENCE 277:955-959(1997).	NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,	TISSUE-KIDNEY;	SEQUENCE FROM N.A.	EUTHERIA; PRIMATES.	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	HOMO SAPTENS (HUMAN).	TELOMERASE REVERSE TRANSCRIPTASE.	(TREMBLREL. 06, LAST	(TREMBLREL. 05,	1998 (TREMBLREL.	O14746 PRELIMINARY; PRT; 1132 AA.	1

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                                      Query Match
Best Local S
Matches 92
                                                                                                            SEQUENCE FROM N.A.

MEDLINE; 97433088.

MEYERSON M., COUNTER C.M., EATON E.N., ELL
CADDLE S.D., ZIAUGRA L., BEIJERSBERGEN R.L
BACCHETTI S., HABER D.A., WEINBERG R.A.;
CELL 90:785-795(1997).

EMBL; AF018167; G2347129; -.
SEQUENCE 1132 AA; 126937 MW; C1E5E2AF
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014783;
014783;
01-JAN-1998
01-JAN-1998
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                                                                                                                                                                                                                                                                                                           SAPIENS (HUMAN)
RYOTA; METAZOA;
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MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW
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                                                          Similarity
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8 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
8 (TREMBLREL. 06, LAST ANNOTATION UPDAT
CATALYTIC SUBUNIT.
                                    97.7%;
larity 99.9%;
Conservative
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                                  Score 6948; DB 4;
Pred. No. 0.00e+00;
0; Mismatches 1
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01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA
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                                                                                                                                                                       RHNERRELRNTKKFISLGKHAKLSLQELTWKMSVRGCAWLRRSPGVGCVPAAEHRLREEI
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                                                                                                                                                      PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
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GREENBERG R.A., ALLSOPP R.C.,
ONCOGENE 0:0-0(1998).
EMBL; AF051911; G3005592; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1122 AA; 127977 M
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LQPYMRQFVAHLQET--SPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYV
                                                   QCQGIPQGSSLSTLLCSLCFGDMENKLFAEVQRDGLLLRFVDDFLLVTPHLDQAKTFLST
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 QCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRT
                                                                                                                                                                                                                                          GTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGD-KEQLRPSFLLSS
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Similarity 61.0%;
574; Conservative
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169; M
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Pred. No. 0.00e+00;
169; Mismatches 163;
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STRAIN=972H-;
MEDLINE; 97400623.
NAKAMURA T.M., MORIN G.B., CHAPI
LINGNER J., HARLEY C.B., CECH T
SCIENCE 277:955-959(1997).
EMBL; AF015783; G2340169; -.
PFAM; PF00078; rvt.
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013339;
01-JAN-1998
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SEQUENCE 989 AA; 116456 MW;
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Local Similarity 26.7%;
les 125; Conservative
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8 (TREMBLREL. 05, LAST 9
8 (TREMBLREL. 07, LAST 4
REVERSE TRANSCRIPTASE )
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8 (TREMBLREL. 05, LAST )
8 (TREMBLREL. 06, LAST )
REVERSE TRANSCRIPTASE
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128; Mismatc
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                                                         T SEQUENCE UPDATE)
T ANNOTATION UPDATE
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2.26e-10
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                                                           SEQUENCE FROM N.A.
MEDLINE; 97274210.
LINGNER J., HUGHES T
CECH T.R.;
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CECH T.R.;
SCIENCE 276:561-567(1997).
SCHENCE 276:561-567(1997).
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EMBL; AF015783; G2340168; -.
EMBL; AL022299; E1185360; -.
PFAM; PF00078; rvt.
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NAKAWIRA T.M., MORIN G.B., CHAPMAN K.B.,
LINGNER J., HARLEY C.B., CECH T.R.;
SCIENCE 277:955-959(1997).
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Local Similarity 26.8%; Pred. No. 9.66e-108;
Les 125; Conservative 125; Mismatches 200; Indels
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DE TELOMERASE CATALYTIC SUBUNIT (FRAGMENT).
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF029235; G2605903; -.
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  RLRFIPK
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                                                                                                 FFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVIDSKN
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51; Conse
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llarity 25.2%;
Conservative
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8368 MW;
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76.1%;
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; Pred. No. 2.78e-58;
122; Mismatches 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
T (FRAGMENT).
                                                                                                                                                                                                Score 424; DB 11;
Pred. No. 1.11e-56;
10; Mismatches 6;
                                                                                                                                                                                                                                                                                                 E2A06F2B CRC32;
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Best Local
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EMBL; U20618;
SEQUENCE 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TREMBLEEL 01, CREATED)
01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLEEL 07, LAST ANNOTATION UPDATE)
CHROMOSOME XII COSMID 8543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHERRY J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C (AB972);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEDLER H., ZIMMERM.
NATURE 387:0-0(0).
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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              501
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                                                                                                                                                                                                                                         QIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF
                                                                                                                                                                                                                                                                                                                    | :| | | : | | : | :| :| : | : :| : ::| : ::| : ::| : ::| :::| :::| :::|
                              E---M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKAS
                                                                                            VR-RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLN
                                                                                                                                            VRSQY-FFNTNT-G-VLKLFNV-VNASRVPKPY-ELYIDNVR-TVHLSNQDVIN---VV-
                                                                                                                                                                                           DI-HRAWRTFVLRV-RA-QDPPPELYFVKVDVTGAYDTIPQ-DRLTEVIASIIKPQNTYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVXVVELLRSFFYVTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLKKLRLKDFRWLFIS-DIWFTKHNFENLNQLAIC-FISWLFRQLIPKIIQTFFYCTEIS
  EASSGLEDVELREMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDM-E-NKLF-AG
                                                                                                                                                                                                                                                                                                                                                                                       FQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHRE-ARPALLTSRLRFIPK
                                                                                                                                                                                                                                                                                           - PDGLRPIVNMDY - VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 4.4%;
1 Similarity 24.3%;
118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JUL-1997) TO EMBL/GENBANK/DDBJ DATA
518; G662136; -.
884 AA; 102662 MW; 1A94320F CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 314; DB 3; Length Pred. No. 3.84e-35; Inde 122; Mismatches 202; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A94320F CRC32;
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Best Local
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01-JUL-1997
01-JUL-1997
01-JUL-1997
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                                                                                                                                                                                                                                                         EMBL; SE
                                                                                                                                                                                                                                                                                                                        AZEN
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MEDLINE; 87284169.

PETIZNER A.J., TSAI E.C., STROMINGER J.L.,
J. VIROL. 61:2902-2909(1987).

EMBL; M17294; G807646; -.

HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN (FRAGMENT).
HUMAN HERPESVIRUS TYPE 4.
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMMAHERPESVIRINAE
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                      AM. J.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 96108975.
                                                                                                                                                                                                                                                                                                                                                                                                               EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. HUM. GENET. 58:143-153(1996)
S80916; G1911492; -.
HPGKPEGPPPQEGNKSKSARSPPGKPQGPPQQEGNKSQGPPPPGGNPQQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK
                                                                                      TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ο̈́.
                                                                                                                                                h 2.0%;
Similarity 28.2%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                     234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%;
llarity 38.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31393 MW;
                                                                                                                                                                                                                                       23656 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04, CREATED)
04, LAST SEQUENCE UPDATE)
04, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 147; DB 14; Pred. No. 6.53e-06; 20; Mismatches 33;
                                                                                                                                                Score 142; DB 4; L
Pred. No. 3.60e-05;
41; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D17CEF6F CRC32;
                                                                                                                                                                                                                                       B5920075 CRC32;
                                                                                                                                                                                                                                                                                                                          PRAKOBPHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HERPESVIRIDAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECK S.H.;
                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 296;
                                                                                                                                                                                                                                                                                                                            NIECE
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     MAMMALIA;
                                                                                                                                                                                             234;
                                                                                                                                                                                                                                                                                                                          R.L.;
                                                                                                                                                     9
                                                                                                                                                     Gaps
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                                                                  258
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RESULT RESULT OF ACCORD OF
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Best Local S
Matches 3
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THESIS (1995), UNIVERSITAET B.
EMBL; X78052; G459248; -.
EMBL; X81893; E258949; -.
SEDUENCE 276 AA; 31718 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q46612;
Q46612;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TT 12
054226
054226;
                                     EMBL; YI
NON_TER
                                                                   SALAH-BEY K., DOUMITH M., MICHEL J.M., HAYDOCK LEADLAY P.F., RAYNAL M.C.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; Y14332; E1228185; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
POLYKETIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
IS 1222 GENE ORF-A AND ORF-B.
                                                                                                                                                                                                                                                                                                                         SACCHAROPOLYSPORA ERYTHRAEA (STREPTOMYCES PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-KLEEBERGER, 1983;
MEDLINE; 95255664.
                                                                                                                                                                                                                    STRAIN-NRRL2338;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEIBL H.D., SIDDAVATTAM D., PLASMID 34:223-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEIBL H.D., LEWECKE F.M.;
GENE 156:37-42(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTEROBACTER AGGLOMERANS
   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLL-RPAAPNLTWSDDFVMDALATGRRIK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRV-QLRELSEAEVRQHREARPALLTSRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITELALERRR-FGYRR-IWQLLRREGLHVNHKRVYRLYHLSGLGVKRRRR-RKGLATERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
30; Conser
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       373
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larity 33.7%;
Conservative
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   A
K
   40872
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   MW;
                                                                                                                                                                               MICHEL J.M., HAYDOCK S., CORTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 141; DB 2; Le
Pred. No. 5.04e-05;
23; Mismatches 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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   781BEC6D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373
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                                                                                                               BANKS
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RESULT 13
ID 036027;
AC 036027;
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DT 01-JUN-
DT 01-JUN-
DE WISKOTT
GN WSP1 OF
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Best Local
                                         ULT 14

Q99076;
Q99076;
C1-NOV-1996 (TREMBLREL 01, C1)
O1-NOV-1996 (TREMBLREL 01, C1)
O1-NOV-1998 (TREMBLREL 05, L1)
O1-JUN-1998 (TREMBLREL 06, L1)
O1-JUN-1998 (TREMBLREL 06, L1)
O1-JUN-1998 (TREMBLREL 06, L1)
HOMEOBOX PROTEIN (FRAGMENT).
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01-JUN-1998
01-JUN-1998
01-JUN-1998
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DOMAIN
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-JS21;
ZANKEL T.C., OW D.W.;
SUBMITTED (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WISKOTT-ALDRICH SYNDROME WSP1 OR SPAC4F10.15C.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO YEAST LAS17.
EMBL; AF038575; G2708709; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                             305 AANKKRPPPPPP-PSRR---NRG-KPPIGNGSSNSSLPPPPPPPRSNAAG-SIPLPPPQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 PPRP 338
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                                                                                                                                                                             321
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                                                                                                                                                                             VGRQHHAGPPSTSRPPRPWDTPCPPV
                                                                                                                                                                                                       VPTPP-SLPPSAPPSLPPSAPPSLPM
                                                                                                                                                                                                                                       RGAAPEPERTPVGQGSWAHP-GRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPS
                                                                                                                                                                                                                                                                 SAPPPPPPRSAPSTGRQPPPLSSSRAVSNPP--APPPAIPGRSAPALPPLGNASRTSTPP
                                                                                                                                                                                                                                                                                              AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR
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42; Conser
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Similarity 32.3%;
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(TREMBLREL.
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337
361
248
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larity 28.8%;
Conservative
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06, LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                MW;
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Pred. No. 2.56e-05;
41; Mismatches 53;
                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                        CREATED)
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L -> V (IN 9
4; 9E84D37C (
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Pred. No. 7.05e-05;
27; Mismatches 46
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POLY-PRO.
                                                                                                                  PRT;
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CRC32;
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Search completed: Fri Dec 18 18:17:04 1998 Job time : 166 secs.
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Best Local Similarity 26.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.9%;
Best Local Similarity 30.9%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN=CD-1; TISSUE=LIVER;

STRAIN=CD-1; TISSUE=LIVER;

MEDLINE: 88273214.

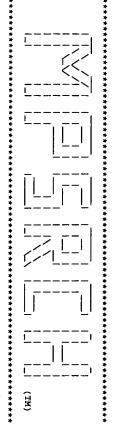
ANN D.K., SMITH M.K., CARLSON D.M.;

J. BIOL. CHEM. 263:10887-10893(1988).

EMBL; M23236; G567232; -.

MCD; MGI:97773; PRP.
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O62103; O1-NOV-1996 (TREMBLREL. 01, CREATED)
O1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
PROLINE RICH PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGUCHI Y., KEHRL J.H.;
NUCLEIC ACIDS RES. 19:3742-3742(1991).
NUCLEIC ACIDS RES. 19:3742-3742(1991).
-I- SIMILARITY: STRONG WITH OTHER "ANTP-TYPE" HOMEOBOX PROTEINS.
EMBL; X56537; E30256; ALT_SEQ.
PIR; S16681; S16681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00046; homeobox.
DNA-BINDING; NUCLEAR PROTEIN; HOMEOBOX; PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-TONSIL; MEDLINE; 91305;
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                                                                                                                                                            154 GGPQPRPPQGPPPPAGPQPRPPQGPPPP 181
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                                                                                                                                                                                                                                      259
                                                                                                                                                                                                                                                                                        95 PPPGGPQPRPPQGPPPPGG-PQPRPPQGPPPPGGPQGPPPPGGPQQRPPQGPPPP 153
                                                                                                                                                                                                                                                                                                                                                                                 HPSVGRQHHAGPPSTSRPPRPWDTPCPP 345
                                                                                                                                                                                                                                   RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPAR-PAEEATSLEGALSGTRHS 317
                                                                                                                                                                                                                                                                                                                                                AATQARPPPHAS--GPRRRLGCE-RAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
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112
316 AA;
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16 317 II
317 AA; 31719 MW;
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121 H
34713 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 132; DB 11; Length 317; Pred. No. 9.90e-04; 38; Mismatches 64; Indels 7;
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H-T-H MOTIF.
1531E766 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
PROLINE-RICH PROTEIN.
10C84341 CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Dec 18 18:34:59 1998;

Run Tabular output not generated. MasPar time 9.57 Seconds 508.951 Million cell updates/sec

Description: Perfect Score: (640-940) from US08951733.pep (2 of 2) 2214 >US-08-951-733-14

Scoring table: PAM 150 TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Gap 11

Post-processing: 131922 seqs, 16180660 residues

Searched:

Minimum Listing Match 0% first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28

Statistics: Mean 34.011; Variance 149.700; scale 0.227

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
109 97 97 97 90 90 90 90 90 90 90 90 90 90 90 90 90	Score
44446000000000000000000000000000000000	Query Match I
370 903 1398 1398 785 785 420 423 421 420 433 935 1784 1784 1784 1784 1784 1784 1784 1784	Length
22 116 227 116 222 222 117 116 116 116 116 117 119	DB
W20923 W241007 W241007 W214124 R87008 W16303 W16303 W215927 W2	ID
H. pylori cytoplasmic Hyperthermostable pro Pyrococcus furiosus p Protease. Yeast mitochondria CO Xenopus melatonin rec Xenopus melatonin rec Xenopus melatonin rec Xenopus melatonis subrinant squirrel High-affinity melaton Fusaric acid resistan Barnacle adhesion pro FeLV F6A provirus clo Gene product of first M.tuberculosis small T. litoralis DNA poly Bacillus subtilis srf gC1q receptor.	Description
2.55e+00 1.85e+01 1.85e+01 1.85e+01 1.85e+01 5.64e+01 5.64e+01 5.64e+01 5.64e+01 5.64e+01 7.72e+01 7.72e+01 7.72e+01 7.72e+01 7.72e+01 7.72e+01 7.72e+01 7.72e+01 7.72e+02 9.01e+02 9.01e+02 9.01e+02 9.01e+02 9.01e+02 9.01e+02	Pred. No.

Query Match 4.9%; Best Local Similarity 25.0%; Matches 17; Conservative

Score 109; DB 22; 1 Pred. No. 2.55e+00; 23; Mismatches 24;

Length 370; Indels

4.

Gaps

4.

45	44	43	42	41	40	39	38	37	36	35 5	34	ω G	32	<u>ω</u>	30	29	28	27	26	25	24	23	22	21	20	Ţ
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Apolipoprotein B-100.	Virulence gene cluste	Deduced sequence of c	Berolina potato starc	Starch binding protei	Cyclomaltodextrin glu		Timothy grass pollen	7	_	\sim	_	Human melanoma associ	HIV virus-1(LAI) gp12	Protease inhibitor.	Human melanoma associ	Plasmodium falciparum	length		Yeast sn-2 acylglycer			NF-ATP.		RING11 antigenic pept	Human RAD51 protein,	Mouse Kappi procein,
				2.25e+02		1.93e+02		1.66e+02		-	1.93e+02			-	1.66e+02		:.	1.93e+02	1.93e+02	3e+0	1.43e+02	1.23e+02	1.43e+02	1.23e+02	1.23e+02	I.ZJETUZ

ALIGNMENTS

The present sequence is a H. pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be H. pylori cytoplasmic protein, 16ae10508orf10.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope. Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter claim 61; Page 1321-1322; 1481pp; English. Berglindh OT, WPI; 97-05230 W20923 standard; protein; W20923; N-PSDB; T68716. 01-APR-1996; 06-JUN-1996; 07-JUN-1995; WO9640893-A1. Helicobacter pylori. isolated from H. pylori by PCR amplification for recombinant production, e.g. in E. coli hosts.
Sequence 370 AA; (ASTR) ASTRA AB. 21-JUL-1997 (first entry) 97-052306/05. US-630405 U09122 US-487032. Smith D, Mellgaerd BL; 370 AA. polypeptide

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Query Match
Best Local
                                                                                                                                             used as :
                                                                                                                                                                   Protease(s) and genes encoding them obtained from Thermococcus and Pyrococcus strains - have extremely high thermal stability and are useful industrially and as research reagents
Disclosure; Page 100-108; 159pp; Japanese.
This sequence represents the protease from Pyrococcus furiosus. This sequence is a protease of the invention. The proteases of the invention have extremely high thermal stability. The proteases can used as research reagents, and industrially in the food, drug and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 2
R87007 standard; Protein; 903
R87007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T95670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsunasawa S, Yamam
WPI; 97-332794/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asada K, Kato I, Mitta M, Tsunasawa S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1997.
07-NOV-1996; J03253.
12-DEC-1995; JP-323285.
(TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus furiosus WO9721823-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease; research reagent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (T08141) from Pyrococcus furiosus. Recombinant proteas is obtd. by cultivation of a transformant prepd. using plasmid carrying the protease gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant prodn. of hyper:thermostable procease Claim 2; Page 43-48; 85pp; Japanese.
Claim 2; Page 43-48; 85pp; Japanese.
A hyperthermostable protease (R87007) is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus furiosus hyper:thermostable purecombinant prodn. of hyper:thermostable
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N-PSDB; T08141.
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05-JUN-1995; J01095.
13-JUN-1994; JP-130236.
26-JUL-1994; JP-173912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyperthermostable protease
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                                                                                                      as research reagents,
ical industries.
ence 1398 AA;
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17; Consea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  furiosus protease.
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29
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Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermal stability; pyrococcus furiosus.
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Pred.
15; M
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97;
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   DB 27;
1.85e+01;
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1.85e+01
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The invention relates to a gene (T08111) that codes for a hyperthermostable protease (R87007) of Pyrococcus furiosus. A related DNA sequence (T08132) includes the coding sequence of the protease gene and encodes a protein (R87008) that
comprising an excised RNA transcript encoded by the group II intron alZ (see also T63319) of the COX1 gene and a protein encoded by the group II intron alZ of the COX1 gene. The RNP is incubated with the DNA substrate in the presence of a divalent cation so that at least one strand of the DNA substrate is cleaved and a nucleic acid molecule is attached to one or both of the cleaved strands. The
                                                                                                                                         Disclosure; Page 40-42; 58pp; English.
Yeast mitochondrial COXI gene intron ail-encoded protein (W16303)
can be used in a novel method for cleaving a double-stranded or
single-stranded DNA substrate. The method utilises a nucleotide
integrase, pref. a (reconstituted) ribonucleoprotein (RNP) particle
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12-SEP-1995; US-526964.
(OHIO-) OHIO STATE RES
                                                                                                                                                                                                                                                                                                                                          Guo H, Lambowitz AM, WPI; 97-202256/18. N-PSDB; T63319.
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                                                                                                                                                                                                                                                                    the cleaved strand
                                                                                                                                                                                                                                                                                          New ribonucleoprotein particle double- or single-stranded DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast mitochondria COX1
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WPI; 96-049674/05.
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26-JUL-1994;
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llarity 29.38;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP-130236.
JP-173912.
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also be u
Sequence
      Claim 5; Page 25-26; 62pp; French.
Sequences W25926-7 represent novel allelic Xenopus laevis melatonin receptor MEL-1A proteins. This sequence is a new form of the melatonin receptor designated MEL-1AA, also known as Mel 1-(clalpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different C-terminal amino acids. The protein is encoded by 2 different alleles (T79063-4) which differ in the 3'
                                                                              New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                      (ADIR ) ADIR & CIE.
Jockers R, Marullo S,
WPI; 97-132635/12.
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Xenopus melatonin receptor; untranslated region; PCR;
Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR;
mRNA; half-life; skin; amplification; primer; polymerase chain reaction;
transmembrane domain; cellular signalling; inhibition; adenylyl cyclase;
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24-JUL-1996; F01167.
24-JUL-1995; FR-008947.
(ADIR ) ADIR & CIE.
Jockers R, Marullo S,
WPI; 97-132635/12.
New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer Claim 5; Rage 30-31; 62pg; French.
Sequences W25926-7 represent novel allelic Xenopus laevis melatonin receptor MEL-la proteins. This sequence is a new form of the melator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus melatonin receptor MEL-IAb.
Allele; Xenopus laevis; melatonin; receptor; untranslated region; PC mRNA; half-life; skin; amplification; primer; polymerase chain react transmembrane domain; cellular signalling; inhibition; adenylyl cycl modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
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5.64e+01;
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T 9
18409 standard; Protein; 420
R88409;
15-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                          The present sequence represents a recombinant squirrel protease inhibitor protein 55RS that contains a specifically claimed reaction site, see features table. The protease inhibitor 55RS has inhibitory activity against trypsin, elastase or thrombin. The protease inhibitor has a new structure similar to alpha-1-antitrypsin and shows selective inhibitory activity against proteases. The protease inhibitor cDNA was homologous to cDNA encoding a similar squirrel protein designated
                                                                                                                                                                                                                                                                                                                                                                                                                                        protease(s)
Claim 4; Page 8-9; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KOND/) KONDO J.
(KANA-) ZH KANAGAWA KAGAKU
WPI; 97-369473/34.
                                                                                                                                                                                                                                                                            hibernation-related protein (HP-55). Sequence 413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squirrel derived protease inhibitor has similar structure to antitrypsin - shows selective inhibitory activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1997.
04-DEC-1995; 315692.
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09-OCT-1997
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                                                                                                                     LRVRAQDPPPELYFVKVDVTGAYD
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larity 45.8%;
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25..413
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Pred. No. 5.(
6; Mismatch
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Pred. No.
13; Misma
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. 5.64e+01;
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5.64e+01;
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High-affinity melatonin receptor.

Melatonin receptor; G-protein-coupled receptor; glycosylation;
disulfide bond; ligand binding pocket; phosphorylation;
cytochrome-c family heme binding site; melatonin receptor-agonist;
melatonin receptor-antagonist; circadian rhythm disorder; jet-lag;
day-night cycle disorder; ovulation; reproductive cycle; antibody;
animal breeding; puberty; transgenic animal; drug screening.
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57..68
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67..72
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33..57
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395
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296..3
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16
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269..279
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                                                                                                               "Protein-kinase-C
                                                                                                                                           "Protein-kinase-C phosphorylation
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                                              "Protein-kinase-C
                                                                               "Protein-kinase-C
                                                                                                                                                                                                                                             "Transmembrane region-VII"
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HERSOLF HERSOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conser
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07-JUN-1995; U07360.
17-JUN-1994; US-261857.
07-OCT-1994; US-31987.
06-JUN-1995; US-319887.
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Fusaric acid resistant genes for acid resistant genes for detoxifying m
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                                                  The sequence was deduced from a clone isolated from a gene library prepal from P. cepacia. It is the 1st of five proteins encoded by ORFs fadA-fadE which are essential for fusaric acid resistance. The protein has a mol. wt. of 47 kD. The genes can be introduced into plants in order to control plant diseases such as wilting disease caused by Fusarium fungi.
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WPI; 96-058
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(DAIK ) DAIKIN IND LTD.
Shibano Y, Toyoda H, Utsumi
WPI; 91-261442/36.
                                                                                                                                                                                                  Claim 18; Fig 4; 38pp; English.
The sequence was deduced from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-1991
28-FEB-1991; 103006
28-FEB-1990; JP-045481.
18-FEB-1991; JP-044027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-444664-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas cepacia, strain UK-1.
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                          See also R13839-R13845.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1991
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llarity 33.9%;
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e.g. Pseud
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Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                                                                   12-DEC-1989; 100871.
13-DEC-1988; US-284139.
(COLS) UNIV COLORADO STATE R
(HARD) UNIV HARVARD.
HOOVEY EA, Mullins JI;
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(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO
WPI; 95-388689/50.
N.-SSDB; T05722.
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J07265081-A.
17-OCT-1995.
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R94427;
R94427;
11-JUN-1996 (first entry)
FeLV F6A provirus clone 61E encoded nucleocapsid FeLV; retrovirus vaccine; AIDS; disease model; i viraemia; leukaemia; therapy; nucleocapsid.
Feline immunodeficiency virus subtype A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnacle adhesion protein gene - for production of adhesive protein Claim 1; Page 7; 7pp; Japanese.
This is the amino acid sequence of the barnacle (Megabalanus rosa) adhesion protein. The corresp. gene was isolated from a cDNA library using the probe T05723 which is derived from amino acid sequencing of the purified protein. The gene is used to produce an adhesive protein which can be used in water.
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R85478
R85478;
                                  immuno-deficiencies in other species, e.g. human.
Disclosure; Fig 1; 22pp; English.
The nucleocapsid protein (R94427) and envelope protein
sequences of feline leukaemia virus provirus F6A clone
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   sequences of feline leukae
deduced from open reading
                                                                                                                                                                              Inactivated FeLV-A sub-type isolates for use in d
vaccines - can be used to study prophylaxis and
                                                                                                                                                                                                                                                              WPI; 96-180826/19.
N-PSDB; T13265.
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06-MAR-1996.
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Local Similarity 24.28;
nes 23; Conservative
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5.63 37;
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5.64e+01
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Best Local 9
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                                                                                                                                                                                  11-NOV-1993.
30-APR-1993; E01063.
30-APR-1992; US-875940.
14-AUG-1992; US-929206.
17-SEP-1992; FR-001098.
16-APR-1993; FR-004545.
(ASSI-) ASSISTANCE PUBLIQUE.
(INSP) INST PASTEUR.
(MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (T13265). Clone 61E is replication competent and capable of inducing persistent viraemia in cats. Host cells, e.g. feline cell can be transformed with DNA derived from 61E and used to produce infectious virus useful in vaccines, in the generation of viraemia and in disease challenge systems.

Sequence 1784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding virus-A sub:type - producing AIDS type disease in cats, used to test drugs and vaccines.
Claim 6; Fig 1.1-17; 23pp; English.
Variant of viral genome induces immunodefficiency in cats similar NaIDS. May be used in research, especially in testing drugs and vaccines against vireamia and and feline leukaemia viruses.
Sequence 1784 AA;
(UYBE-) UNIV BERNE.
(UYPA-) UNIV CURIE PARIS VI P & M.
BODMET T. COLE S, Heym B, Honor
Young D, Zhang Y;
WPI: 93-368812/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9322454-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                streptomycin; antibiotic; susceptibility; sensitive; resistar rpsL; mutant; small ribosomal subunit; S12 ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R51371 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1042 lafenirka-llsspalglpditkpfelfi 1070
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Hoover EA, Mullins JI;
WPI: 90-218326/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1990.
12-DEC-1989; 122964.
13-DEC-1988; US-284139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feline
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R05898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harvard Univ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%;
Similarity 36.7%;
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Pred. No. 7.
9; Mismatc
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Pred. No.
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                                                                               Honore N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents T. litoralis DNA polymerase. The DNA CC sequence encoding this protein contains introns decribed in the Specification, however this protein sequence appears to be translated through these intronic sequences. Only a portion of the DNA CC plymerase protein sequences. Only a portion of the DNA CC plymerase protein sequence is reproduced in the specification. The CC intoralis DNA polymerase gene sequence may be derived from the bacteriophage NEB #619 on an approx. 14kb BmmHI restriction fragment. CC when this gene is transformed in to E. coli and expressed in its CC entirety, it is found to be unstable. There is a high frequency of mutation in the polymerase gene, cell growth is slow and there is some degree of cell mortality. This instability is due in part to the presence of the two introns. It is thought that the intervening DNA in this sequence encodes a separate protein which may be spliced out at the protein level. The second, 1170bp, intron has been found to cold for an endonuclease which self splices out in E. coli. To improve stability of the DNA when it is expressed in E. coli, the Specification states that it is desirable to delete the introns of the expression vector into E. coli.
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Best Local S
Matches 1
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Example 2; Fig 14; 97pp; English.
The rpsL gene of M.leprae encodes the S12 protein of the small ribosomal subunit that is responsible for resistance to streptomycin. Two primers were designed based on this sequence and were used in a PCR amplification of M.tuberculosis DNA. Sequence analysis of the 306bp amplified fragment showed 28 differences between the rpsL gene from M.leprae (Q5153) and M.tuberculosis (Q61454). In streptomycin resistant strains, a single amino acid substitution due to a mutation in codon 43 (wild-type AAG mutated to AGG) was identified; substitution of Lys42 by Arg results in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-1992; 311622.

18-DEC-1991; US-811421.

(NEWE ) NEW ENGLAND BIOLABS

Comb DG, Jack WE, Kucera F

WPI; 93-198889/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase; intron; translation; bacteriophage NEB #619; E. mutation; cell growth; endonuclease; self splicing; stability; expression; transformation; expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R38095
R38095;
                                                                                                                                                                                                                                                                                                                                                                                           Recombinant thermostable DNA polymerase from archaebacteria expressed efficiently by removal of intervening introns Claim 1; Fig 19; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q43515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; Q61454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-547920-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermococcus litoralis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1994 (first entry)
T. litoralis DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         resistance to streptomycin. Sequence 102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rapid detection
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les 16; Conser
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llarity 24.2%;
Conservative
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R, Perler
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Pred.
21; M
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Query Match Best Local S

h 3.9%; Similarity 28.6%; 22; Conservative

Score Pred. 19; M

e 86; DB 8; Lei . No. 1.05e+02; Mismatches 28;

Length 1702; 2; 28; Indels

8

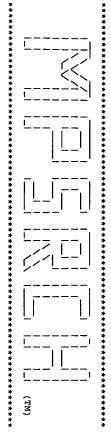
Gaps

7;

- Db 1132 dgklvwkpvpyymrhra 1148 : |: :|:|| Qy 708 IHR-AWRT--FVLRVRA 721

Search completed: Fri Dec 18 18:35:58 1998 Job time : 59 secs.

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Dec 18 18:36:16 1998; MasPar time 12.67 Seconds 811.235 Million cell updates/sec

Tabular output not generated.

Title: >US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

Description: Perfect Score: Sequence: TSRLRFIPKPDGLRPIVNMD.....NLRKTVVNFPVEDEALGGTA 301

Searched: PAM 150 Gap 11 107076 seqs, 34141958 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir56 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 47.293; Variance 102.661; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Result
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1.84e-06 1.3.12e-01 1.3.12e-01 1.1.20e-00 2.01e-00 1.57e-00 2.04e+00 2.04e+00 2.04e+00 2.04e+00 2.04e+00 2.04e+00 2.04e+00 3.43e+00 3.43e+00 3.43e+00 3.43e+00 3.73e+00	Pred. No.

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F69195	OKBYN2	HJNVAV	I56333	A31070	·C28821	F64045	S56487	ADSPAC	F69117	CFXCA	S03701	E64222	E64170	G70189	A53467	A69873	S45346	151247	F65076	S73466	S17995
cell surface glycopro	protein kinase GCN2 (helicase (EC 3.6.1)	apolipoprotein B - ra	6-phosphofructokinase	1-phosphatidylinosito	excinuclease ABC, cha	hypothetical 40.4K pr	fructose-bisphosphate	conserved hypothetica	C-phycoerythrin alpha	141K protein - pea ea	topoisomerase IV chai	hypothetical protein	threoninetRNA ligas	protein kinase SNF1 h	phosphate starvation	fructose-bisphosphate	aldolase C - African	hypothetical protein	probable DNA primase	gene COX1 intron 1 pr
2.54e+01	2.54e+01	2.54e+0	2.54e+01	2.54e+0	2.54e+0	2.54e+0	2.54e+01	2.54e+0	2.54e+0	2.54e+01	1.56e+01	1.22e+01	1.99e+0:	1.56e+01	1.56e+01	1.99e+01	1.56e+01	1.56e+01	1.56e+0:	1.99e+01	7.38e+00

ALIGNMENTS

VΩ	В	Qy	당	Qy	망	Qγ	及	Qy	ઠ	Que Bes Mat	SUMMARY	# •	#dene	CENER				# # O O	. #= . 03	# 20	REFERENCE	DATE	ORGANISM	ALTER	TITLE	RESULI
918 C	698 A	861 T	638 A	801 H	593 N	743 P	539 P	686 Ý	481 I	Query Match Best Local Matches	MARY	##cro	#gene	##exp	##cro	##residues	##mol	#description #accession	#submission	#authors	ENCE		ISM	ALTERNATE_NAMES		T 1
VVNLRK'	KANRDK	FICSIC:	PIVDLY	LQETSP	VR-TVH	Q-DRLTI	RMECMR	LNYERA	LEYLRN	ch 1 Simi 68;		ss-ref		erimen	ss-ref	idues	ecule_	b		_						_
CVVNLRKTV-VNEPVEDEAL 936	AKANRDKILAVSSQSDDDTV 717	TLLCSLCYGDM-E-NKLF-AGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYG	DDLLEFY	HIQETSPLRDAVVIEQSSSINEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILS	SNODVI	EVIASII	PRMECMR-ILKDALKNENGFFVRSQY-FFNTNT-G-VLKLFNV-VNASRVPKPY-ELYID	VLNYERARRPGLIGASVIGIDDI-HRAWRTFVLKV-RA-QDPPPELYFVKVDVTGAYDTI	ILEYLRNKRPTSF-TKIYSPTQIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSI 538	/ Match 6.7% Local Similarity 26.2% ses 68; Conservative	#length 884	##cross-references SGD:S0004310; MIPS:YLR318w	SGD:EST2	cal_sour	##cross-references EMBL:U20618; NID:g2258165; PID:g662136; MIPS:YLR318w	1-6	##molecule_type DNA	The sequence of S. cerevisiae cosmiq 8545. S53396	submitted to the EMBL Data Library,	Du, 2.	S53390	03-may-1993 *sequence_revision vi-sep-1998	#formal_name	cerevisiae) hypothetical	hypothetical protein YLR318w -	1000
EDEAL	VIDDO:	KLF-AG	SEFKASI	ÖSSSİNI	γγ- ₋ -	PONTYC	NENGFF	SYLGLDI	KIYSPT	6.7%; 26.2%; cvative		SGD:S0	-	ce str	EMBL: U	84 ##1		lence of	id to t			1998	name Sa	.ical p	ical p	‡
936	717	IRRDGLL	PSQDTLI	EASSGLE	- X-	VR-RYAV	VRSQY-F	DI-HRAW	QIADRI-	Score Pred. 67;	#molecular-weight 102662	004310;		ain 528	20618;	1-884 ##label DUZ		S. Ce	TEWE D			ganence	Saccharomyces cerevisiae) protein L8543.12	1 protein YLR3	
		LRLYDDF	LKLADDF	DVFLRFM	EIF-K-T	VQKAAHG	FNTNT-G	RTFVLRV	KEFKQRL	Score 148; DB 2; Length 884; Pred. No. 1.84e-06; 67; Mismatches 93; Indels 32;	ar-weig	MIPS:Y		вс (Аву	NID:922	2		revisia	Data L			T 67 79 7	nyces c	L8543.1	YLR318w	
		LLVTPHI	LIISTDO	CHHAVRI	ALW	HVRKAFE	-VLKLF1	-RA-QDI	LKKFNN	DB 2; 84e-06; hes 9;	ht 1026	LR318w		(2)	58165;			e cosma	ibrary,			0 L	erevisi	2		
		THAKTE	INIAÖÖ	ERGKSYV	/EDKCYI	SHVSTL	W-VNAS	PPELYE	LPELYF	Length					PID:g6			0 8545	February			sep-199	lae		st (Sac	
		LRTLVRG	KKLAMGG	QCQGIPC	REDGLFC	TDLOPYN	RVPKPY-	VKVDVTG	MKFDVKS	884; els 32	#checksum				62136;			٠	ary 1995			, , ,	7		yeast (Saccharomyces	
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##molecule_type DNA
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# #length 94 #molecular-weight 10659
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Local Similarity 26.8%;
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                                                                                             Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.;
Sutton, G.G.; Fleischmann, R.D.; Ketchum, K.A.; Klenk,
H.P.; Gill, S.; Dougherty, B.A.; Nelson, K.; Quackenbush,
J; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.;
McKenney, K.; Fitzegerald, L.M.; Lee, N.; Addams, M.D.;
Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Uterback, T.R.;
Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.;
Fujli, C.; Bowman, C.; Watthey, L.; Wallin, E.; Hayes,
W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
C.M.; Venter, J.C.
Nature (1997) 388:539-547
The complete genome sequence of the gastric pathogen
Helicobacter pylori.
erences MID:97394467
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                                                                             A64591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP-binding protein - Helicobact #formal_name Helicobacter pylori 09-Aug-1997 #sequence_revision 0
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                       preliminary; nucleic acid sequence not shown;
translation not shown
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g protein - Helicobacter pylori (strain 26695)
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Pred. No. 3.12e-01;
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19; Mismatches 30;
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#cross-references MUID:97426617
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##cross-references GB:AE000571; G
TIGR:HP0569
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##experimental_source
                                                                      ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-189 ##label BAD 1-189 ##cross-references EMBL:246659; NID:g575680; PID:g575683; MIPS:YML036w
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                                 ##cross-references GB:AE000225; GB:U00096; NID:g1787523; PID:g1787531;
                                                                                           ##status
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Similarity 25.8%;
16; Conservation
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Similarity 26.1%;
                                                                                                               G64875
                                                                                                                                                                      Science (1997) 277:1453-1462
                                                                                                                                                                                                       Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shav
                                                                                                                                                                                                                                                                                                                                      664875 #type complete
aconitate hydratase (EC 4.2.1.3) - Escherichia coli
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
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                                                                                           nucleic acid sequence not shown;
                                                      1-891 ##label BLAT
                 UWGP: b1276
strain K-12, substrain MG1655
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the EMBL Data Library, November 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 103;
Pred. No. 1.
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21; Mismatches
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Rose, D.J.; Mau, B.; Shao,
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##molecule_type protein
""-~~**dnes 'X',3-15,'X',17,'X',19 ##label
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                                  ##residues 1-891 ##label MEN
##cross-references GB:L22081; NID:g348943; PID:g348945

Carbon-oxygen lyase; hydro-lyase
#length 891 #molecular-weight 98208 #chec
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                                                                                                               ##molecule_type DNA
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Local Similarity 21.9%;
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aconitate hydratase (EC 4.2.1.3) - Legionella pneumophila
#formal_name Legionella pneumophila
03-May-1994 #sequence_revision 03-May-1994 #text_change
09-Sep-1997
                                                                                                                                                                     Mengaud, J.M.; Horwitz, M.A.

J. Bacteriol. (1993) 175:5666-5676

The major iron-containing protein of Legionella pneumophila is an aconitase homologous with the human iron-responsive element-binding protein.
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J. Gen. Microbiol. (1991) 137:2505-2515
The aconitase of Escherichia coll: purification
and molecular cloning and map location of the
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Eur. J. Biochem. (1992) 204:599-609
The aconitase of Escherichia coli. Nucleotide sequence of
aconitase gene and amino acid sequence similarity with
mitochondrial aconitases, the
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##note the nucleotide sequence was submitted to the EMBL Dat
Library, February 1994
#length 205 #molecular-weight 23260 #checksum 7617
                                                                                                                                                                                                            165
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##note the nucleotide sequence was submitted
Library, April 1995
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1-205 ##label ESP
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Similarity 22.1%;
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                            reverse transcriptase like protein 1, in alga (Pylaiella littoralis) (fragment) #formal_name Pylaiella littoralis 29.Nov 1995 #sequence_revision 01-Mar-1990 01-Mar-1996
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Esposito, D.; Scocca, J.J.
Mol. Microbiol. (1994) 13:885-695
Identification of an HPl phage protein
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#formal_name phage HP1
06-Dec-1996 #sequence_revision 13-Mar-1997
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Pred. No. 1.57e+00;
49; Mismatches 50
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22; Mismatches 23;
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#title
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Bauthors Boyd, A.; Kendall, K.; Simon, M.I.
#journal Nature (1983) 301:623-626
#title Structure of the serine chemorecep
#cross-references MUID:83141753
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                                                                                                                                                                                                          ##molecule_type DNA
##residues_ 1-503,'X',505-551 ##label BUR
1-503,'X',505-551 ##label BUR
##cross-references EMBL:U14003; NID:g1263172; PID:g537197
##note the nucleotide sequence was submitted to the
#note Library, August 1994
                                 ##molecule_type DNA
##residues 1-147,'STSSLISRPRDIRN',162-536 ##label
##cross-references GB:V00373; GB:J01718; NID:g43217; pJ
2NCE S30279
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UWGP:b4355
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##residues 1-59
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Local Similarity 46.7%;
hes 14; Conservative
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The mitochondrial LSU rDNA of the brown alga Pylaiella littoralis reveals alpha-proteobacterial features and littoralis reveals alpha-proteobacterial features and
                                                                                                                                                                                                                                                                                                                                                                                                                         Blattner, F.R.
Nucleic Acids Res. (1995) 23:2105-2119
Analysis of the Escherichia coli genome VI:
the region from 92.8 through 100 minutes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science (1997) 277:1453-1462
The complete genome sequence of Escherichia nces_MUID:97426617
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methyl-accepting chemotaxis protein I (MCP-I)
#formal_name Escherichia coli
14-NOV-1983 #sequence_revision 13-Feb-1998 #text_change
Roper, D.I.; Fawcett, T.; Cooper, R.A. Mol. Gen. Genet. (1993) 237:241-250
                                                                                                                         A03442
                                                                                                                                                                                                                                                                                                                                                                                   S56581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burland, V.; Plunkett III, G.; Sofia, H.J.;
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th 318 #checksum 7326
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Pred. No. 1.57e+00;
7; Mismatches 8;
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Best Local
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#journal
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##molecule_type DNA
##residues 1-7
                  #accession $20168
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This protein responds to changes in serine concentration in the
environment, transduces a signal from the outside to the inside
of the cell, and facilitates sensory adaptation through various
levels of methylation.
                                                                                                                                                          ##cross-references EMBL:X05143; NID:g4019; PID:g4020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 EKQYVAYMEQNDRLHDIAVSDNNASYSQAMWILVGVMI 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737 GAYDTIPQD-RLTEVIASIIKPQ-NTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPY 794
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                                                                                                                                                                                             ##molecule_type DNA
##residues 1-184 ##label SLO
                                                                                                                                                                                                                                                                                                ##cross-references EMBL:U19104; NID:g609423; NCE S15581 .
                                                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
##residues 1-1114 ##label
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Similarity 22.48;
22; Conservation
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99 min
                                                     Labouesse, M.; Herbert, C.J.; Dujardin, G.; Slonimski, P.I
EMBO J. (1987) 6:713-721
Three suppressor mutations which cure a mitochondrial RNA
maturase deficiency occur at the same codon in the open
reading frame of the nuclear NAM2 gene.
                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, December 1994 The sequence of S. cerevisiae cosmid L3502. $51470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein L3502.2
#formal_name Saccharomyces cerevisiae
23-Feb-1995 #sequence_revision 12-May-1995
                                                                                                                                                                                                                                       Slonimski, P.P. submitted to the EMBL Data S20170
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chemotaxis; methylated amino acid; sensory transduction;
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                                     MUID:87218532
translation not shown
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#modified_site glutamate methyl
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#modified_site glutamate methyl ester
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cheB-dependent deamidation and methylation) #status
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h 551 #mol
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Pred. No. 2.04e+00;
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REFERENCE
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Best Local Similarity 40.8%;
Matches 20; Conservative
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286-778
                          1133-1151
1160-1179
                                                                                                  736-753
756-778
779-1187
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211-285
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#journal Mol. Gen. Genet. (1988) 213:297-309
#title Divergence of the mitochondrial leucyl tRNA synthetase genes
in two closely related yeasts Saccharomyces cerevisiae and
Saccharomyces douglasii: a paradigm of incipient evolution.
#cross-references MUID:89039717
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#map_position 12R
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##mosidues 1-62 ##label HER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid sequence not shown; translation not shown ##molecule_type genomic RNA ##nabel DUP ##abel DUP ##abel DUP ##cross-references EMBL:X15062
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##residues 1-61 ##label LAB
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                                                                                                                                                                                                                                                                                                                                                                                                   the nucleotide sequence was submitted to the EMBL Data Library, April 1989, in computer-readable form #superfamily yellow fever virus genome polyprotein; capsid protein; envelope protein; glycoprotein; nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dupuy, A.; Despres, P.; Cahour, A.; Girard, M.; Bouloy, M. Nucleic Acids Res. (1989) 17:3989

Nucleotide sequence comparison of the genome of two 17D-204

yellow fever vaccines.

nces MUID:89282413

S07757
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E; nonstructural protein NS1; nonstructural protein NS2a;
nonstructural protein NS4a; nonstructural protein NS4a;
nonstructural protein NS4a; nonstructural protein NS4b;
nonstructural protein NS5
#formal_name yellow fever virus
31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                 protein; polyprotein; transmembrane protein
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                          #domain transmembrane #status predicted #label TM5\
#domain transmembrane #status predicted #label TM6\
                                                                                                                                                                           #domain transmembrane #status predicted #label TM2\
#product major envelope protein E #status predicted
#label MEE\
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#domain transmembrane *status predicted *label TMI\
#product envelope protein M *status predicted *label
                                                                        #product nonstructural protein NSI #status predicted #label NSI\
                                                                                                                          #domain transmembrane #status predicted #label TM3\
product nonstructural protein NS2a #status predicted
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1355-1484	1159-1180 1188-1354	740-753 755-778 779-1187	249-269 271-285 286-778	2-210 211-285	d Mr	#cross-refere	#journal #title	ACCESSIONS REFERENCE #authors	ORGANISM DATE	RESULT 12 ENTRY TITLE CONTAINS	Qy 885 LLRLV	MLV	Db 1334 GLTQPF : Qy 826 GLFDVF	Query Match Best Local Simil Matches 21;	SUMMARY	134,150,172,594, 908,986,1796,2066, 2320,2346,2408, 2467,2720,2734, 2740	2507-3411	2395-2506	2108-2394	1485-2107	1355-1484
		#domain transmembrane #status predicted #label TM3\ #domain transmembrane #status predicted #label TM4\ #product nonstructural protein NS1 #status predicted #label NS1\	#domain transmembrane #status predicted #label TM1\ #domain transmembrane #status predicted #label TM2\ #product major envelope protein E #status predicted #label MEE\	#product capsid protein C #status predicted #label CPC\ #product envelope protein M #status predicted #label	: 1-3411 ##label RIC #superfamily yellow fever virus genome polyprotein capsid protein; envelope protein; glycoprotein; nonstructural protein; polyprotein; transmembrane protein	nces MUID:85272570 A03914	Science (1985) 29:726-733 Science (1985) 29:726-733 Nucleotide sequence of yellow fever virus: implications for flavivirus gene expression and evolution.	A03914 A03914 Rice, C.M.; Lenches, E.M.; Eddy, S.R.; Shin, S.J.; Sheets,	l_name yellow feve -1985 #sequence_re pr-1996	GNWYY #type complete genome polyprotein - yellow fever virus (strain 17D) capsid protein C; envelope protein M; major envelope protein E; nonstructural protein NS1; nonstructural protein NS2a; nonstructural protein NS2b; nonstructural protein NS3; nonstructural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5	889	1396	LTQPFLG-LCAFLATRIFGRRSIPVNEALAAAGLVGVLAGLAFQEMEN-FLGPIAVGGL 1391 : : :: : : : ::	4.6%; Score 101; DB 1; Length 3411; ilarity 32.3%; Pred. No. 2.04e+00; Conservative 14; Mismatches 27; Indels 3; Gaps 3;	#length 3411 #molecular-weight 379528 #checksum 8417	#	#product nonstructural protein NS5 #status predicted #label NS5\				•

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KEYWORDS acyltransferase
SUMMARY #length 372 #moloc
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                                                                           Query Match 4.5%;
Best Local Similarity 34.0%;
Matches 18; Conservative
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Best Local S
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594,755,908,986,
1796,2062,2320,
2346,2408,2467,
2720,2734,2740
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                                                                                                                                                                                                 ##molecule_type DNA
#residues 1-372 ##label BUL
##cross-references GB:U67570; GB:L77117; NID:g1591929; PID:g1591936;
##cross-references GB:MJ1298; PID:g1511307
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  729
                          296 YEFIKEDNLTPIYPFIFKEKTMEIAEHLIK-NNIFCVGIRYPTVPKGLE-RIR 346
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  Y-FVKVD-VTGAYDTIPQDRLTEVIASIIKPQNTYCV-RRYAVVQKAAHGHVR 778
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Similarity 32.3%;
21; Conservative
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Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
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                                                                                                                                                      acyltransferase
#length 372  #molecular-weight 41895  #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #formal_name Methanococcus jannaschii
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
10-Oct-1997
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                                                                           Score 99; DB 2; 1
Pred. No. 3.43e+00;
11; Mismatches 19
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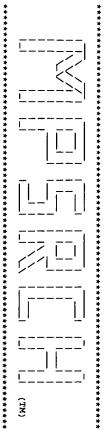
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                                                                                                                                                                                                                 ##molecule_type mRNA
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##cross-references EMBL:M92421; N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  676 LTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDV 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 LAAGVNALASHLQAEQAEN-DLLQARLIGSSEAERS-R-IALDLH-DEMGPQLFALRAAV 258 | : | : | : | : | : | : : : | : | : : : |
                                                                                                                                                      ##rcsidues 1-557 ##label ADJ
##cross-references EMBL:X66695; NID:g9511; PID:g9512
# #length 557 #molecular-weight 62921 #ch
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                                        33 RIKMFMPRAYELKVTVIKMAFELSTRCSKRDGVVETVLTDVIEGK-TMSGYDRSGRVNLL
                                                                                     Match 4.5%;
Local Similarity 25.0%;
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  RLR-FIPKPDGLR-PIVNMDYVVGARTFRREKRAER-LTSRVKALFSVLNYERARRPGLL
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Similarity 21.7%;
35; Conservative
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
09-Sep-1997
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#length 446 #molecular-weight 48236 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harms, N.; Reijnders, W.N.M.; Anazawa, H.; van der Palen, C.J.N.M.; van Spanning, R.J.M.; Oltmann, L.F.; Stouthamer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory protein moxY - Paracoccus denitrificans
                                                                               Conservative
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                                                                           Score 100; DB 2; Le
Pred. No. 2.65e+00;
21; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99; DB 2; I
Pred. No. 3.43e+00;
55; Mismatches 60
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:37:17 1998; MasPar time 9.66 Seconds 836.466 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: Sequence: >US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 49.063; Variance 85.433; scale 0.574

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 20 21 23 23	14 15 17 18	132 132 133 133	Result No:
999993 9223 444) V V V V V V V V V V V V V V V V V V V	103 105 103 102 102 101 101 101 101 101 100 98 98	Score
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YGFG_ECOLI YAO6_SCHPO UUP1_HAEIN PARC_MYCGE PHSG_YEAST	VP23_HSV11 ALFC_CARAU ASPG_METJA AI2M_YEAST Y010_MYCPN	YMD6_YEAST ACO1_ECOLI ACON_LEGPN YOO1_BPHP1 RMCP1_ECOLI RH18_YEAST POL6_YEFV1 POL6_YEFV2 MOXY_BADDE YEO2_SCHPO0 YCF1_YEAST ACON_BRAJA PTDJ MOUSE	IJ
HYPOTHETICAL 49.2 KD P HYPOTHETICAL 49.1 KD P ABC TRANSPORTER ATP-BI TOPOISOMERASE IV SUBUN GLYCOGEN PHOSPHORYLASE	CAPSID PROTEIN VP23. ERUCTOSE-BISPHOSPHATE PROBABLE L-ASPARAGINAS PUTARIVE COX1/OX13 INT HYPOTHETICAL PROTEIN M	HYPOTHETICAL 20.7 KD P ACONITATE HYDRATASE 1 ACONITATE HYDRATASE (E HYPOTHETICAL 23.2 KD P METHYL-ACCEPTING CHEMO DNA REPAIR PROTEIN (CO GENOME POLYPROTEIN (CO	Description
4.24e+00 5.67e+00 5.67e+00 3.16e+00 3.16e+00	1.74e+00 2.35e+00 1.74e+00 5.67e+00	2.00e-01 1.06e-01 2.09e-01 2.75e-01 3.76e-01 3.76e-01 3.76e-01 3.76e-01 5.14e-01 9.52e-01 9.52e-01	Pred. No.

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357 366 428 4428 4433 7609 7789 7789 7789 7789 7789 7789 7789 77	1117 124 164 297
	4444
ALE_SPIOL YJGF_ECOLI MLIC_XENLA DDI1_YEAST FUSA_BUNCE LAFE_VIBPA YHA2_YEAST YHA2_YEAST YHA2_YEAST YHA2_YEAST YHA2_YEAST FRA1_GCOLE RR12_HORVU TRM8_ECOLLI RR12_CCLEER RR12_CCLEER RR12_CCLEER RR12_CCLEER RR12_CCLEER RR12_CCLEER RR12_CCCLEER	YDVG_SCHPO RR12_EUGGR PHEA_FREDI YQXG_BACSU VIRB_SHIFL
FRUCTOSE-BISPHOSPHATE HYPOTHETICAL 40.4 KD P MELATONIN RECEPTOR TYP DNA-DAMAGE INDUCIBLE P FUSARIC ACID RESISTANC FLAGELLAR HOOK ASSOCIA HYPOTHETICAL 51.2 KD P EXCINUCLEASE ABC SUBON 1-PHOSPHATIDYLINOSITOL 6-PHOSPHATIDYLINOSITOL	PUTATIVE HELICASE C6F1 CHLOROPLAST 30S RIBOSO G-PHYCOERYTHRIN ALPHA HYPOTHETICAL 32.5 KD P VIRULENCE REGULON TRAN
7.00e+01 7.00e+01 1.00e+01 1.00e+01 1.00e+01 1.00e+01 1.00e+01 1.00e+01 7.56e+00	5.67e+00 7.56e+00 7.56e+00 1.00e+01

ALIGNMENTS

R R R	8888		RESULT ID A AC P	Qy Db	g g	Z MO	SO RE REP	SS SS DT TO ACC	RESULT
(1) SEQUENCE FROM N.A. MEDLINE; 92174916.	ACNA OR ACN. ESCHERICHIA COLI. PROKANYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS; ENTEROBACTERIACEAE.	(REL. 22, (REL. 35, (REL. 35, YDRATASE 1	ULT 2 ACOL_ECOLI STANDARD; PRT; 890 AA. P25516; P78060; P78148; O1-MAY-1992 (REL. 22. CREATED)	108 KFH-TNT-DDVDKEQLRTIMTSIVKGQE 133 : :: :: : 732 KVDVTGAVDTIPQDRLTEVIASIIKPQN 759	50 GEQMYSAIYKTLIEV-KYNKMRTRNLNSECVLCLSPTSNISDAF-LKFGIKDDSSQLICL 107 	Query Match 4.7%; Score 103; DB 1; Length 181; Best Local Similarity 26.1%; Pred. No. 2.00e-01; Matches 23; Conservative 25; Mismatches 35; Indels 5; Gaps 5;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-S288C / AB972; BADCOCK K., CHURCHER C., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; BADCOCK K. (CHURCHER C., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (NOV-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; Z46659; G575683; ALT_SEQ. HYPOTHETICAL PROTEIN. SEQUENCE 181 AA; 20662 MW; AC111C34 CRC32;	YMD6_YEAST STANDARD; PRT; 181 AA. Q03705; Q1-NOV-1997 (REL. 35, CREATED) Q1-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) Q1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) HYPOTHETICAL 20.7 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION. YMLD36W. SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). SUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.	1

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RESULT
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Best Local Similarity 21.9%;
Matches 14; Conservative
                                                                      ACON_LEGPN STANDARD; PRT; 891 AA. p37032; 01-JUN-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE) ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE HYDRO-LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
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ECOGENE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRODROMOU C., HAYNES M.J., GUEST J.R.;
J. GEN. MICROBIOL. 137:2505-2515(1991).
-!- FUNCTION: MAY HAVE AN IRON-RESPONSIVE REGULATORY FUNCTION.
-!- CATALYTIC ACTIVITY: CITRATE - CIS-ACONITATE + H(2)O.
-!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SUBUNIT: MONOMER.
-!- SUBUNIT: MONOMER.
-!- SUBUNITABE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE (3FE-4S)
-!- THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE INTERCONVERTS CITRATE, CIS-ACONITASE, AND ISOCITRATE.
-!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12;
AIBA H., BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYASE; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000225; G1787531; -.
EMBL; D90765; G1742087; -.
EMBL; D90766; G1742090; -.
EMBL; S22375; S22375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMURA S., KITAGAMA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI MOTOWIRA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLATTNER F.R., PLUNKETT
SUBMITTED (JAN-1997) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-K12 / MG1655;
BLATTNER F.R., PLUNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X60293; G40896;
  LEGIONELLA PNEUMOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBMITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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                                                                                                                                                                                                                                                                                                                                                                                                                       643
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                                                   MAJOR IRON-CONTAINING
                                                                                                                                                                                                                                                                                                                   703
                                                                                                                                                                                                                                                                                                                                                                   811 LPLE
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                                                                                                                                                                                                                                                                                                                   GTD
                                                                                                                                                                                                                                                                                                                                                                                                                       LRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASV 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E; PS00450; ACONITASE_1; 1.
E; PS01244; ACONITASE_2; 1.
TRICARBOXYLIC ACID CYCLE; IRON-SULFUR; 4FE-4S.
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EM. 204:599-609(1992).
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97516 MW;
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                                                   PROTEIN) (MICP) (IP210).
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EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 105;
Pred. No. 1.
22; Mismatc
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(BY SIMILARITY).
G -> S (IN REF. 2).
; 276673F6 CRC32;
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(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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.06e-01
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Best Local Similarity 25.08;
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STRAIN-PHILADELPHIA 1;
MEDINIE; 93374864.
MENGAUD J.M., HORWITZ M.A.;
J. BACTERIOL. 175:5666-5676 (1993).
J. BACTERIOL. 175:5666-5676 (1993).
J. BACTERIOL. 175:5666-5676 (1993).
J. BACTERIOL. 175:5666-2676 (1993).
J. BACTERIOL. 175:56666 (1993).
J. BACTERIOL. 175:566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
ESPOSITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YOO1_BPHP1 STANDARD; PRT; 205 AA. P51700; P51700; O1-OCT-1996 (REL. 34, CREATED) O1-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE) O1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) HYPOTHETICAL 23.2 KD PROTEIN IN INT-C1 INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                    ESPOSITO D., FITZMAURICE W.P., BENJAMIN WALDMAN A.S., SCOCCA J.J.; WALDMAN A.S., SCOCCA J.J.; EDGE COLOR RES. 24:2360-2368(1996).
EMBL; U24159; G459176; ENGLEMENT OF TRANSMEMBRANE. PROTEIN; TRANSMEMBRANE. TRANSMEM 12 32 POTENTIAL. TRANSMEM 49 69 POTENTIAL.
                                                                                                                                                                                              SEQUENCE
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PROSITE; PS01244; ACONITASE_2; 1.
LYASE; TRICARBOXYLIC ACID CYCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; LEGIONELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-HP1C1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-HP1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIRIDAE; DS-DNA NONENVELOPED VIRUSES; MYOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIOPHAGE HP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRYQENQQDLVIIAGKEYGTGSSR-DWAAKGTNLLG-VKAVITE-SFERIHRSNLIGMGI 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROBIOL. 13:685-695(1994).
4.6%;
Similarity 22.1%;
33; Conserva+***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95089704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96279738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            706
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                                                                                                                                                                                          205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOCCA J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435
                                                                                                                                                                                          69 P
23260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98209 MW;
         Score 102; DB 1; Le
Pred. No. 2.75e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRON (IRON-SULFÜR CLUSTER)
(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 103; DB 1;
Pred. No. 2.00e-01
                                                                                                                                                                                          POTENTIAL.
821C7A9F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6230AC5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.C.,
                                                                                                                                                                                              CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOODMAN S.D.,
                                                                                                 Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 891
                  Indels
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                  17;
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         Gaps
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    MEDLINE; 8220
KEHRY M.R., DAHI
TOL. CHEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P02942; P76817;
21-JUL-1986 (REL. (
01-JUL-1993 (REL. 2
15-JUL-1998 (REL. 3
                                                                                                                                                                                                                                  SEQUENCE OF 295-317 AND 483-507, AND MEDLINE; 82265699.
                                                                                                                                                                                                                                                                                                                                   STRAIN-K12 / MG1655;
MEDLINE; 95334362.
BURLAND V.D., PLUNKETT G. III, SOFIA H.J., DANIELS D.L.,
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG165
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 83141753.
BOYD A., KENDALL K., SIMON
NATURE 301:623-626(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCP1
                                                                                                                                                                                                                                                                                         STRAIN-C;
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-77 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                            ENTEROBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                    ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHYL-ACCEPTING
                                                                                                                                                                                        POST-TRANSLATIONAL MEDLINE; 91236753.
                                                                                                                                                                                                                                                                      ROPER D.I.,
                                                                                                                                                                                                                                                                               MEDLINE; 93204900
                                                                                                                                                                                                                                                                                                                            BLATTNER F
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN)
                                                                                                                                                                                                                                                                                                                    NUCLEIC ACIDS RES. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         709
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                                                                                                                                                                                                                                                             GEN. GENET. 237:241-250(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRAWRTFVLRV-RAQDPP-PELY-FVKVDVTGAYDTIPQDRLTEVI-A-SIIKPQNTYC- 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KEYNAIQLKIFWDIEHSLSTLYMFDKSN-KQEIDTILGYLLKDINSATSLIEKHARYDE 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLSTLIIMCFTAVGVMSWKKQKTPD-LKSKV-AK-NIIDFD-TH-AVLLPSKKFQSIDEI 106
                                                                                                                                                                                                                 DAHLQUIST F.W.;
EM. 257:10378-10386(1982).
                                                                                                                                                                                                                                                                      FAWCETT T., COOPER R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEMOTAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01, CREATED)
26, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
CHEMOTAXIS PROTEIN I (MCP-I)
                                                                                                                                                                                                 MODIFICATIONS
                                                                                                                                                                                                                                                                                                 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551
                                                                                                                                                                                                                                             POST-TRANSLATIONAL MODIFICATIONS
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RESULTATION OF THE PROPERTY OF
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Best Local :
                                                                                                                                                                                               SEQUENCE FKUM N.S.

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., LIVE J., KUC FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUC FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN D., JOHNSON D., HALLSWORTH K., HAWKINS J., HILLER L., LE T., MARDIS E., MICHAELSWORTH K., HAWKINS J., LATRETILLE P., LE T., MARDIS E., MICHAELSWORTH K., HARDIS E., MICHAELSWORTH M., PELUSO D., RIFKEN L., RILES GRECO T., WOHLDMAN P.,
                                                                                                                            MILLER N., NHAN M., PAULEY A., PELUS TAICH A., TREVASKIS E., VIGNATI D., WILSON R., WATERSTON R.; SUBMITTED (JAN-1995) TO EMBL/GENBANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RH18_YEAST STANDARD; PRT; 1114 AA 012749; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDAT DNA REPAIR PROTEIN RHC18 (RAD18 HOMOLOG). RHC18 OR YLR383W OR L3502.2.
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SEQUENCE
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PROSITE; PSO
CHEMOTAXIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96069417.
LEHMANN A.R., WALICKA M., GRIFFITHS I
MCCLERADY S., CARR A.M.;
MOL. CELL. BIOL. 15:7067-7080(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECO2DBASE; B060.7;
ECO2DBASE; B060.8;
ECOGENE; EG11034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECO2DBASE; B060.3;
ECO2DBASE; B060.4;
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ECO2DBASE; B0
                                                            STRAIN-AB1-4A/8/55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                               SEQUENCE OF 1-184 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 EKQYVAYMEQNDRLHDIAVSDNNASYSQAMWILVGVMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737 GAYDTIPQD-RLTEVIASIIKPQ-NTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPY 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 ADYEALPRDPRQSTAAAAEIKRNYDIYHNALAELIQLLGAGKINEFF-DQ-PTQGYQDGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          795 MRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFL
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   HERBERT C.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANE;
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   DUJADIN G., SLONIMSKI P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 1;
Pred. No. 3.76e-01
28; Mismatches 4
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THE 3 ARG MAY FORM A POSITIVELY CHARGED POCKET, WHICH BINDS THE ALPHA-CARBOXYL GROUP OF THE ATTRACTANT AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2A, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
RNA POLYMERASE (EC 2.7.7.48) (NS5)).
YELLOW FEVER VIRUS (STRAIN 17D).
YIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
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COTENCE 229:726-733(1985).
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DOMAIN
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                                                                                                                                                                                                                PIR; A03914; GNWVY.
POLYPROTEIN; GLYCOPROTEIN;
                                                                                                                                                                                                                                        PROTEIN M AND GLYCOPROTEIN E. THE PROTEIN C AND MRNA.
EMBL; X03700; G59339; -.
EMBL; K02749; G336193; -.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 85272570.
                                                                                                                                                                                                                                                                                                                                                                                                                                     FLAVIVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLG_YEFV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -I- FUNCTION: ACTS IN A DNA REPAIR PATHWAY FOR RE DNA DAMAGE THAT IS DISTINCT FROM CLASSICAL NU REPAIR AND IN REPAIR OF IONIZING RADIATION DA -I- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-I- SIMILARITY: BELONGS TO THE SMC FAMILY.
2MBL; X80930; E198113; -
2MBL; U19104; G609425; -
2MBL; U19104; G609425; -
2MBL; X05143; G4020; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           795
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                                                                                                                                                                                                                                                                           FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION. NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION. SUBUNIT: THE VIRLON OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRQFVAH-LQETSPLRDA--VVI-EQSSSLNEASSGLFD-VFLR-FMCH
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35 39 NUCLEAR LOCALIZATION SIGNAL
109 116 ATP (POTENTIAL).
259 529 COILED COIL (POTENTIAL).
696 969 COILED COIL (POTENTIAL).
1114 AA; 128008 MW; BC94F87E CRC32;
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                 NONSTRUCTURAL PROLL.
NONSTRUCTURAL PROLL.
HELICASE (NS3).
HENOTEIN NS4A.
TONSTRUCTURAL PROTEIN NS4B.
TOLYMERASE
                                                                                                                                                                                                    RNA-DIRECTED RNA POLYMERASE; TEIN; HELICASE; ATP-BINDING;
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Pred. No. 3.76e-01;
                                                                       ENVELOPE GLYCOPROTEIN M.
MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2B.
                                                                                                                                                               REMOVED FROM CAPSID PROTEIN CELLULAR AMINOPEPTIDASE.
           RNA-DIRECTED RNA POLYMERASE POTENTIAL.
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                                                                                                                                                                                                     TRANSMEMBRANE;
                                                                                                                                                                                                                 CORE PROTEIN
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P19901;
01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
PROTEINS NS1, NS2A, NS2A, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
RNA POLYMERASE (EC 2.7.7.48) (NS5),
YELLOW FEVER VIRUS (STRAIN PASTEUR 17D-204).

VIRIDAB; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; FLAVIVIRIDAE;
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                                                                                                                                                                                                                                           EMBL;
PIR;
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                                                                                                                                                                                COAT PROTEIN;
                                                                                                                                                                                                                    PIR; S07757; GNWVYP.
POLYPROTEIN; GLYCOPROTEIN;
                                                                                                                                                                                                                                                                                                                      DUPUY A., DESPRES P., CAHOUR A., GIRARD M., BOULOY M.;
NUCLEIC ACIDS RES. 17:3989-3989(198).
NUCLEIC ACIDS RES. 17:3989-3989(198).
PERMIC FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAN REPLICATION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAN REPLICATION.
ON THE VIRAN REPLICATION.
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 89282413.
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TEIN; HELICASE;
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Pred. No. 3.76e-01;
14; Mismatches 27;
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ENVELOPE GLYCOPROTEIN M.
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NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
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01-APR-1993 (REL. 25, LAST SE
01-FEB-1995 (REL. 31, LAST AN
METHANOL UTILIZATION CONTROL
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01-APR-1993
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HARMS N., REIJNDER
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                                                                     TRANSMEMBRANE;
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SPANNING R.J.M., OLIMANN L.F., STOUTHAMER A.H.;
MICROBIOL. 8:457-470(1993).
MICROBIOL. 8:457-470(1993).
FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM MOXY/MOXX
PROBABLY INVOLVED IN THE REGULATION OF THE METHANOL DEHYDROGENASE
EXPRESSION. MAY EUNCTION AS A MEMBRANE-ASSOCIATED PROTEIN KINASE
THAT PHOSPHORYLATES MOXX IN RESPONSE TO ENVIRONMENTAL SIGNALS.
                                                                                                                                                          (PROBABLE).
SIMILARITY: TO OTHER PROKARYOTIC
                                                                                                                                          KINASES
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                                                                                                                         M92421; G150595; -.
                                                                    2871; S32871.
TRANSDUCTION; TRANSFERASE; KINASE; PHOSPHORYLATION;
MBRANE; INNER MEMBRANE; METHANOL UTILIZATION.
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Similarity 32.3%;
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Pred. No. 3.76e-01;
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O13799;
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
                                         SUBMITTED (MAR-1992) TO EMBL; X99720; E264527; -PIR; S19381; S19381, HYPOTHETICAL PROTEIN. SEQUENCE 586 AA; 6515
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01-MAY-1992
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P25579;
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-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE SKI2 SUBFAMILY OF HELICASES.
EMBL; 298597; E334274; -.
EMBL; 298597; E334274; -.
HYPOTHETICAL PROTEIN, HELICASE; ATP-BINDING; NUCLEAR PROTEIN.
HYPOTHETICAL PROTEIN; HELICASE; ATP-BINDING; NUCLEAR PROTEIN.
                                                                                                                                                              SEQUENCE FROM N.A. FULLER L.J., KELLY
                                                                                                                                                                                                                               SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
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                                                                                                                                                                                                                                                                                                        HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAC17H9.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTATIVE HELICASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 LAAGVNALASHLQAEQAEN-DLLQARLIGSSEAERS-R-IALDLH-DEMGPQLFALRAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPIKSLSN-OKY-RELLSEFGDVGLMTGDVSINPSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPPAKTYPFELDPFQSTAIKCVERMESVLVSAHTSAGKTVIAEYAIAQ-ALKNRQRVIYT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AELVTGFRDVAS-ETRVVLDVDPEVEGSSPGELAELSIYRF
::|: :: : : : : : : : : : : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQFVAHLQETSPLRDAVVIEQSSSLNEASSG-LFDVFL-RF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYM 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFK 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHA-QAMTAD-LPERPAALDETLDAIAGHALEV-QRSARTAI-NDLRPMLLGEASLAELL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 4.5%;
Similarity 22.7%;
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 4.5%;
Similarity 21.7%;
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 1
238 2
1030 AA;
                                                                                                                                                                                                                                                                                                   (REL.
(REL.
(REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNGI;
                                                                                                                                                              KELLY
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 36, CREATED)
. 36, LAST SEQU
. 36, LAST ANNO
E C17H9.02 IN C
                                                                                                                                                                                                                                                                                                      22, CREATED)
22, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
KD PROTEIN IN PBN1-APA1 INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                65152 MW;
                                                                                                                                     TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118460 MW;
  4.48;
                                                                                                                                                                                                                                                                                                        PROTEIN IN PBN1-APA1 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE UPDATE)
ANNOTATION UPDAT
IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 100; DB 1;
Pred. No. 5.14e-01;
25; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
55; M
Score 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVH BOX
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                              56434E7A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB34C59C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; DB 1;
No. 7.00e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1030 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          586
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  B
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  1;
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                                                                                                                                                                PEARSON B.M.;
  Length 586;
                                                                                                                                             BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.A., WOOD V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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Query Match

DOMAIN

ETA.

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RRSULT
DT OCCUPATION OF THE PROPERTY OF THE PR
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Best Local :
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                               PTPJ_MOUSE STANDARU;

064455;

01-NOV-1997 (REL. 35, CREATED)

01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)

01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (ED. 1997)

PROTEIN-TYROSINE PHOSPHATASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P70920;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THONY-MEYER L., KUNZLER P.;

J. BACTERIOL. 178:6166-6172(1996).

-:- CATALYTIC ACTIVITY: CITRATE = CIS-ACONITATE + H(2)O.

-:- PATHWAY: TRICARBOXYLIC ACID CYCLE.

-:- SUBUNIT: MONOMER (BY SIMILARITY).

-:- ACONITASE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE (3FE-4S) FORMS.

THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE CATALYTIC SITE THAT
                    SEQUENCE FROM N.A.
STRAIN-MRL-LPR/LPR;
MEDLINE; 96140699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ACONITATE HYDRATASE (EC 4.2.1.3) (CITRATE HYD
                                                                                                                                               MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00450; ACONITASE_1; 1. PROSITE; PS01244; ACONITASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=110SPC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRADYRHIZOBIUM JAPONICUM.
  KURAMOCHI S., MATSUDA S.,
                                                                                                                        EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHIZOBIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    826 LPLTFEEGTSWSSLGLK 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             769 MKYQQEQVPLVVFAGAEYGNGSSR-DWAAKGTRLLG-VRAVIC-QSFERIHRSNLVGMGV 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703
                                                                                                                                                                                                                                                                                                                                                                                                 <u>ц</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCONVERTS CITRATE, CIS-ACONITASE, AND ISOCITRATE.
SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASV 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGLD-DIHRAWRTFVLR 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U56817;
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17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                        RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G1666698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35,
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22.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
  MATSUDA Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98; D
Pred. No. 9.
24; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 9.52e-01;
19; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
24FD4901 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
IRON (IRON-SULFUR CLUSTER)
(BY SIMILARITY).
                                                                                                                                                 VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CITRATE HYDRO-LYASE) (ACONITASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON-SULFUR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  906
  SAITOH T., OHSUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; 9.52e-01
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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-! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: EXPRESSED IN EVERY TISSUE EXAMINED.

-!- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAI-

-!- SIMILARITY: CONTAINS 8 FIBRONECTIN TYPE III-LIKE DOMAINS.
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-!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O
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                                               h 4.4%;
Similarity 28.8%;
15; Conservative
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                                               Score 97; DI
Pred. No. 1.:
18; Mismatcl
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FIBRONECTIN TYPE-III.
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Best Loc
Matches
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P53448;
01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
FRUCTOSE-BISPHOSPHATE ALDOLASE C (EC 4.1.2.
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P10202;
01-MAR-1989
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EMBL; X14112; G59518; -.
EMBL; X14112; E312332; -.
PIR; I30083; WMBET8.
COAT PROTEIN.
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MEDLINE; 90264854.

RIXON F.J., DAVISON M.D., DAVISON A.J.;

J. GEN. VIROL. 71:1211-1214(1990).
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01-MAR-1989 (REL. 10,
01-DEC-1992 (REL. 24,
CAPSID PROTEIN VP23.
                                                                                                                                                                                                                                                                                                                                 CARASSIUS AURATUS (GOLDFISH).
EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
                                  MEDLINE; 93019027.

DAVISON M.D., RIXON F.J., DAVISON A.J.;

J. GEN. VIROL. 73:2709-2713(1992).

-i- FUNCTION: MAY BE A COMPONENT OF TRIMERIC STRUCTURES LINKING

ADJACENT CAPSOMERES AT THE CAPSID SURFACE.

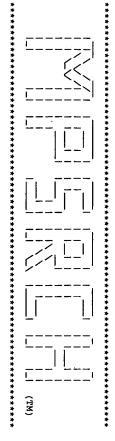
-i- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP23.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 88274327.
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VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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Similarity 34.2%;
27; Conservative
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   HOMOTETRAMER (BY
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LAST SEQUENCE UP
LAST ANNOTATION
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Pred. No. 1.74e+00;
16; Mismatches 28
                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; PISCES; CYPRINIFORMES
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: 4.1.2.13)
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                                                                                                                  GLYCERONE:
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                                                                                                   Query Match
Best Local :
                                                                                                                                     SEQUENCE
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                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                         -i- IN VERTEBRATES, THREE FORMS OF THIS UBIQUITOUS
ARE FOUND, ALDOLASE A IN MUSCLE, ALDOLASE B IN
C IN BRAIN.
-i- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOS
                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                        BINDING
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                                                                                                                                                                                                                                                                         PROSITE;
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                                            712
                                                         147 WRS-VLKI-SETSPSELAIMENANVLARYASICQQNGIVPIVEPEILPDGDHDLKRCQYV
  769
                      205 TEK 207
                                                                                        y Match 4.3%;
Local Similarity 25.4%;
hes 16; Conservative
 VOK
                                            U36777; G1143277;
E; PS00158; ALDOL
                                                                                                                                                                                                                                      SCHIFF BASE; GLYCOLYSIS; MULTIGENE FAMILY.
ET 0 0 BY SIMILARITY.
5 55 C-1-PHOSPHATE GROUP OF
                                                                                                                                    362
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                                                                                                                                    A
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                                                                                                                                                                       362
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                                                                                                                                     XE;
                                                                                                                                                                                                                                                                         _CLASS_I; 1.
                                                                                        Score 95; DB 1; Le
Pred. No. 2.35e+00;
22; Mismatches 20;
                                                                                                                                    AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.; 24B98F89 CRC32;
                                                                                                                                                                                                     (BY SIMILARITY).
C-1-PHOSPHATE GROUP
(BY SIMILARITY).
                                                                                                                                                        SCHIFF-BASE WITH DIHYDROXYACETONE-P
(BY SIMILARITY).
ESSENTIAL FOR ENHANCED ACTIVITY OF T
ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPH
                                                                                                              Length 362;
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                                                                                          Indels
                                                                                                                                                                                                                                                                                                                               GLYCOLYTIC ENZYME
LIVER, & ALDOLASE
                                                                                                                                                                                                                                        THE
                                                                                                                                                            ACTIVITY OF THE 1,6-BISPHOSPHATE
                                                                                                                                                                                                                  THE
                                                                                                                                                                                                                  SUBSTRATE
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                                                                  204
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Search completed: Fri Dec 18 18:37:42 1998 Job time: 25 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:39:23 1998; MasPar time 3.38 Seconds 629.739 Million cell updates/sec

Tabular output not generated.

>US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

Description:
Perfect Score:
Sequence: 1 TSRLRFIPKPDGLRPIVNMD.....NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 31.637; Variance 143.394; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 7 7 6 6 8 8 8 11 11 11 11 11 11 11 11 11 11 11	Result No.
97 97 98 99 90 90 90 81 81 79 79 79 79 80 80 80	Score
44440000000000000000000000000000000000	Query Match I
1398 1398 433 433 890 890 951 1178 1178 1171 567 567 567 567 567 567 567 567 567 567	Length I
444844844844444444444444444444444444444	Ba
US-08-750- US-08-750- US-08-526- US-07-661- US-08-145- US-08-145- US-08-199- PCT-US93-0 PCT-US94-1 US-08-457- US-08-457- US-08-457- US-08-457- US-08-457- US-08-328- US-08-328- US-08-328- US-08-328- US-08-328- US-08-328- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394- US-08-394-	ΙĐ
Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli	Description
Applicatio	, ; ; ; ;
6.92e+00 8.14e+00 2.13e+01 4.65e+01 7.38e+01 7.38e+01 8.59e+01 8.59e+01 8.59e+01 8.59e+01 8.59e+01 1.16e+02 1.16e+	Pred. No.

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PCT-US94-0	US-08-271-	PCT-US93-0	PCT-US94-0	US-08-261-	PCT-US93-0	PCT-US93-0	PCT-US93-0	us-07-762-	US-08-459-	US-08-553-	US-07-829-	US-08-421-	US-07-994-	PCT-US95-0	PCT-US96-0	PCT-US96-0	5212286-2	US-08-268-	US-08-453-	5212286-4	00 00 104
Sequence '	Sequence :	Sequence :	Sequence :	Sequence	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence :	Sequence (Patent No.	Sequence :	Sequence :	Patent No.	ordarine a
48, Applicati	 Applicatio 	l3, Applicati	39, Applicati	Applicatio	Applicati	ll, Applicati	21, Applicati	Applicatio	Applicatio	 Applicatio 	•	Applicatio	Applicatio	Applicatio	 Applicati 	62, Applicati	S	38, Applicati	38, Applicati	Ų.	1 / 1 / 1 / 1 / 1 / 1 / 1 / 1 / 1 / 1 /
1.35e+02	1.35e+02	1.57e+02	1.35e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	1.35e+02	1.35e+02	1.57e+02	1.57e+02	1.57e+02	1.57e+02	F. 000.04

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ALIGNMENTS

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APPLICATION NUMBER: JF 194/173912 FILING DATE: 26-JUL-1994 ATTORNEY/AGENT INFORMATION: NAME: BROWDY, ROGER L.	APPLICATION NUMBER: JP 1994/130236 FILING DATE: 13-JUN-1994 PRIOR APPLICATION DATA:	7 5 H	APPLICATION NUMBER: US/08/750,532 FILING DATE: CLASSIFICATION: 435	S	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible		Washington D.C.	ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Suite 300	R OF SEQUENCES: 18 SPONDENCE ADDRESS:	乭	APPLICANT: ASADA, Kiyozo		APPLICANT: MITTA, Masanori APPLICANT: YAMAMOTO, Katsuhiko		Sequence 1, Application 05/08/50532 Patent No. 5756339	. ,		XXXXXX		LT 1 US-08-750-532-1 STANDARD; PRT; 903 AA.

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Best Local Similarity 29.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08750532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-750-532-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    743 FYLRYKYDVEGLEPGLYVGRIIIDDPTTPVIEDEILNTIVIPEKFTPENNYTLTWYDI 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08750532 Patent No. 5756339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                715 FYLRYRAQ-DP-PPELYFYKYDYTGAYDT-IPQDRL-TEVIASIIKPQNTYCYRRYAY 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 903 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DENCE 903 AA; 100242 MW; 4683955 CN;
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1994/173912
FILING DATE: 26-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MITTA, Masanori
APPLICANT: YAMAMOTO, Katsuhiko
APPLICANT: MORISHITA, Mio
APPLICANT: ASADA, KIYOZO
APPLICANT: ASADA, KIYOZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                              APPLICATION NUMBER: JP 19 FILING DATE: 13-JUN-1994
                                                                                                                                    APPLICATION NUMBER: PCT/JP95/01095 FILING DATE: 05-JUN-1995
                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 20004
                        NAME: BROWDY, Roger L. REGISTRATION NUMBER: 2
            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                 APPLICATION NUMBER: US/08/750,532
                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     E: BROWDY AND NEIMARK, P.L.L.C. 419 Seventh Street N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                               TSUNASAWA, Susumu
KATO, Ikunoshin
                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                            JP 1994/130236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25,618
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Pred. No. 6.92e+00
                       25,618
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            MITTA-1
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Best Local Similarity
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                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                          REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08526964
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08526964 Patent No. 5698421 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 FYLRYRAQ-DP-PPELYFYKYDYTGAYDT-IPQDRL-TEVIASIIKPQNTYCYRRYAY 768
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Local Similarity 29.3%;
hes 17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                               MOLECULE TYPE:
HYPOTHETICAL: NUMBER 185 AA; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 1398 AA; 154545 MW; 10958156 CN;
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Guo, Huātao
APPLICANT: Yang, Jian
TITLE OF INVENTION: Nucleotide Integrase Preparation
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1398 amir
TYPE: amino acid
STRANDEDNESS: si
                                                                TOPOLOGY:
                                                                                     TYPE: amino acid
                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      STREET: 800 Supe
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                ZIP: 44114
                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                LENGTH:
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800 Superior Avenue
                                                                                                785 amino acids
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                                                                linear
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202) 737-3528
                                NO
90390 MW; 3218308
                                                                                                                                                                                                                                                                                         Floppy disk
                                                    peptide
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Pred. No. 6.92e+00;
 Score 96; DB 1; 1
Pred. No. 8.14e+00;
                                                                                                                                                                   22727/00127
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                                 CN;
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           Length 785;
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Patent No.

GENERAL INFORMATION:

CORRESPONDENCE ADDRESS:

US-07-661-610C-2

STANDARD;

Matches

12;

Conservative

7;

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ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5992645man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEPHONE: (703)486-2347
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07661610C
                                                                                                                                                                                              |: |:|| || :|| 644 RFIPKPDGLRPIVNMDY-VVGARTFRREKRAERLTSRVKALFSVL 687
                                                                                                                                                                                                                                       333 RLPPRPDRLRQRAGRAAAIVGAHRKRPPHRSERLAAHAQ-LMAAL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shibano, Yuji
APPLICANT: Toyoda, Hideyoshi
APPLICANT: Utsuni, Ryutaro
APPLICANT: Obata, Kazuaki
TITLE OF INVENTION: Fusaric Acid Resistant Genes
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
NENCE 433 AA; 45666 MW; 736928 CN;
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                                                                                                                                                                                                                                                                                Score 90; DB 1;
Pred. No. 2.13e+01
9; Mismatches 1
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                                                                                                                                                                                                                                                                                                                           Length 433;
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Best Local S
Matches 1
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                                                                                                                               Sequence 5, Application US/08145006C
Patent No. 5656452
GENERAL INFORMATION:
APPLICANT: Rao, Arapplicant: Hogan,
                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application PC/TUS9400545 GENERAL INFORMATION:
                                                               Sequence 5, Application US/08145006C Patent No. 5656452
                                                                                                                                                                                                                                                                                                                                                    664 ARTFRREKRAERLTSRVKALFS-VLNYERARRPGLLGASVLGLDDIHRA 711
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2 Model 502 or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fraser, Janis K.
REGISTATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08, FILING DATE: October 29 APPLICATION NUMBER: 08, FILING DATE: February 1 APPLICATION NUMBER: 08, APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NF-ATP, A T LYMPHOCYTE TITLE OF INVENTION: DNA-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TOPOLOGY: linear
TOE 890 AA; 96929 MW; 4192360 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 18-JAN
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Similarity 38.8%;
19; Conservative
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Hogan, Patrick Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (617) 542-8906
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                         Rao, Anjana
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08/017,052
ary 11, 1993
08/006,067
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Pred. No. 4.65e+01;
13; Mismatches 11
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MEDIUM TYPE: Floppy

ZIP: 22202 CITY: Arlington STATE: Virginia

Virginia

APPLICATION NUMBER: UPPLICATION NUMBER: UPPLICATE: 19910228

CLASSIFICATION: 435

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Query Match Best Local (

Match 4.18; Local Similarity 35.68;

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SEQUENCE

SEQUENCE CHARACTERISTICS: LENGTH: 433 amino acid

433 amino acids

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TYPE: ami

amino acid

linear

Matches

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PCT-US94-00545-5

STANDARD;

McCaffrey, Patricia

NF-ATP, A T LYMPHOCYTE

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Best Local Similarity 38.8%;
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                                                                                                                                       Sequence 23, Application US/08202389 Patent No. 5536636
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 2.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55sx
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/145,006C
APPLICATION NUMBER: US/08/145,006C
FILING DATE: October 29, 1993
                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/017,052
FILING DATE: February 11, 1993
APPLICATION NUMBER: 08/006,067
FILING DATE: January 15, 1993
ATTORNEY/AGENT INFORMATION:
                                             APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
                                                                                                 APPLICANT:
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LENGTH: 890
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NF-ATP, A T LYMPHOCITITLE OF INVENTION: DNA-BINDING PROTEIN
                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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             ADDRESSEE:
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TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K
REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                      Conservative
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E: Hamilton, Brook, Two Militia Drive
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                                                                                               Freeman Jr., Robert M.
Plutzky, Jorge
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Pred. No. 4.65e+01
13; Mismatches 1
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           Smith & Reynolds, P.
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                                                                                                                                                                                                              Sequence 2, Application PC/TUS9307213 GENERAL INFORMATION:
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Local Similarity 22.9%;
les 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 GQVHKTKEQF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                  TITLE OF INVENTION: NUC:
TITLE OF INVENTION: SEQU-
TITLE OF INVENTION: HUM-
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                     APPLICANT: The Government of the United States of APPLICANT: America, as represented by The Secretary TITLE OF INVENTION: NUCLEIC ACIDS AND AMINO ACID TITLE OF INVENTION: SEQUENCES FOR A STRONGLY IMMUNOREACTIVE PROTEIN ENCODED TITLE OF INVENTION: HUMAN HERPESVIRUS 6 STRAIN Z29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein JENCE 95 AA; 11151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 31-JAN-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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         ADDRESSEE: The Government of the unite ADDRESSEE: America, as represented by STREET: 6011 Executive Blvd., Suite 32 CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 28-FEB-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
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TOPOLOGY: linear
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                                                                    The Government of the United States of
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Pred. No. 7.38e+01;
23; Mismatches 28;
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                                                     The Secretary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 LSKRKPDY 81
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07213
FILING DATE: 19930730
        APPLICATION NUMBER: US/08, FILING DATE: CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION: NAME: Plumer, Elizabeth R.
                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks, P.C
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                       APPLICANT: Brenner, Michael B. APPLICANT: Parker, Christina N TITLE OF INVENTION: NO. 559411 NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 858 AA; 95614 MW; 3689832 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/923,743
FILING DATE: 31-UULY-1992
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 496-7056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 858 amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                         COUNTRY: U
ZIP: 02210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                 STATE:
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REGISTRATION NUMBER:
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Similarity 20.6%;
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                         us/08/199,776
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Pred. No. 8.59e+01;
22; Mismatches 29
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5594120el integrin alpha subunit
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             Query Match
Best Local
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Best Local
  Matches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1178 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9502044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-02044-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             718 RVRAQDPPPEL-YFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     631 RIRASTVAPGLQYFG-MSMAGGFD-ISGDGLADITVGTLGQAVVFRSR 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9502044
                                                                                        TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1178 amino acids
             Match 3.7%;
Local Similarity 27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Local Similarity 27.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
TITLE OF INVENTION: Novel integrin alpha subunit
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: BOTELECOMMUNICATION INFORMATION: 617-720-3500
                                        TOPOLOGY: linear
MOLECULE TYPE: protein
MENCE 1178 AA; 129714 MW; 7185561 CN;
                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02044
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield and Sacks,
                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                               FILING DATE: 18 February 1994
ATTOREY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    STREET: 600 At CITY: Boston STATE: MA
                                                                                  LENGTH: 1178 amino acids TYPE: amino acid
                                                                                                                                                                   REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7020
                                                                                                                                                                                                                                                      FILING DATE: h
                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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  13;
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1178 AA; 129714 MW; 7185561 CN;
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  Conservative
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Score 81; DB 2;
Pred. No. 8.59e+01
14; Mismatches 1
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Pred. No. 8.59e+01;
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   Indels
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Best Local Similarity 30.4%;
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                       Sequence 4, Application US/08457646A
                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application PC/TUS9410261A
                                                                                                                                             871 MENKL-FAGIRRDGLLLRL-VDDFLLVTP-HLTHAKTFLRTLVRGVPEY-GCVVNL 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     718
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Sequence 4,
                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 224-07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Carter, William G. APPLICANT: Gil, Susanna A. APPLICANT: Ryan, Maureen C.
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for TITLE OF INVENTION: Integrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVRAQDPPPEL-YFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVR 764
                                                                                                                                                                                                                                        NECULE TYPE: protein

DESCRIPTION: E170 protein as translated from sequence of

DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R

NCE 1713 AA; 189304 MW; 15276084 CN;
                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/FILING DATE: 02-SEP-1994 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98101-8100
                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Shelton, Dennis K. REGISTRATION NUMBER: 26,997
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                  ENGTH:
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Application US/08457646A
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                                                                                                                                                                                                                                                                                                                   1713 amino acids
                                                                                                                                                                                                                                                                                           linear
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, 224-0779
NO: 24:
                                                                                              STANDARD;
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Pred. No. 8.59e+01;
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Best Local Similarity 25.0%;
Matches 8; Conservative
                                                                    Sequence 4, Application US/08458076A
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                                                                                                                                               US-08-458-076A-4
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                             909 LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTA 940
                                                                                                                                                                                                                  141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172
                      Sequence 4, Application Patent No. 5698425 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/457,20
FILING DATE: 01-70N-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Genes for the synthesis o
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
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                                                                                                                                                                                                                                                                                                                                         LENGTH:
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567 AA; 65037 MW; 1552397 CN;
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Schupp, Thomas
Ligon, James M
                                                                                                                                                                                                                                                                                                                                                                             919-541-8689
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Lam, Stephen Ting
Hammer, Phillip E
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Beck, James Joseph
Hill, Dwight Steven
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                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ciba-Geigy Corporation
                                               US/08458076A
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                                                                                                                                                                                                                                          Score 79; DB 1;
Pred. No. 1.16e+02
13; Mismatches 1
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Best Local S
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
TYPE: amino acids
                                                                                                           Sequence 4, Application US/08258261B
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                                                                                                                                                                                                                                      141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172
                                                                              Sequence 4; Application US/08258261B Patent No. 5639949
                                                                            Patent No.
                                                                                                                                                                                                                                                                    y Match 3.6%;
Local Similarity 25.0%;
hes 8; Conservative
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APPLICATION NUMBER: US 08/457,20
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/458,076A
FILING DATE: 01-UN-1995
CLASSIFICATION: 435
DELICATION TOWNSER: US/08/458,076A
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
DENCE 567 AA; 65037 MW; 1552397 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genes for the synthesis of TITLE OF INVENTION: antipathogenic substances NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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Uknes, Scott Joseph
VENTION: Genes for the synthesis of
           Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
 Gaffney, Thomas Deane
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Hill, Dwight Steven
                                          Ligon, James M.
                                                     Schupp, Thomas
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Stephen Ting
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 08/457,205
                                                                                                                                                                                                                                                                                                                                                                                                                  36,129
eR: CGC 1506/CIP3
                                                                                                                                                                                                                                                                              Score 79; DB 1; 1
Pred. No. 1.16e+02
                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                              567
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                                                                                                                                                                                                                                                                                        Length 567;
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RESULT
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Best Local Similarity 25.0%;
Matches 8; Conservative
                                                                                                                                                                                               Sequence 4, Application US/08457342
                                                                                                                                                                                                                                                                      US-08-457-342-4
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                   909 LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTA 940
                                                                                                                                                                                                                                                                                                                               141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172 |::: || || |::: |:::: |:
                                                                                                                                                             Sequence 4, Application US/08457342 Patent No. 5662898
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 919-541-861
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acid
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Releacure Application Data:
APPLICATION NUMBER: US/C
FILING DATE: 08-JUN-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                          TÓPOLOGY: linear
MOLECULE TYPE: protein
UENCE 567 AA; 65037 MW; 1552397 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genes for the sTITLE OF INVENTION: antipathogenic NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                      TITLE OF INVENTION:
                                                       APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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Hammer, Philip Land Wishes, Scott Joseph Uknes, Scott Joseph VENTION: Genes for the synthesis of Trention: antipathogenic substances
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Hammer, Phillip E.
Uknes, Scott Joseph
VENTION: Genes for the synthesis
                                                    Ryals, John Andrew
Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip E.
                                                                                                   Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
                                                                                                                                     Schupp, Thomas
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                                                                                                                                                                                                                                                                      STANDARD;
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Pred. No. 1.16e+02;
13; Mismatches 1:
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Search completed: Fri Dec 18 18:39:40 1998 Job time : 17 secs.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 36,129
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELEPHAN: 919-541-8689
INFORMATION FOR SEQ I NO: 4:
SEQUENCE CLARACTERISTICS:
LENGTH: 567 amino acids
TYPE: protein
SEQUENCE S67 AA; 65037 MM; 1552397 CN;
                                                                                                                                                                         Query Match 3.6%;
Best Local Similarity 25.0%;
Matches 8; Conservative
                                                                                                            141 LLQAAIKYGCKVHQKTTVTEYHADKDGVAVTT 172 | ::: | | | | :: : ::: |:
                                                                                        909 LVRGVPEYGCVVNLRKTVVNFPVEDEALGGTA 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
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                                                                                                                                                                    Score 79; DB 1; Length 567; Pred. No. 1.16e+02; 13; Mismatches 11; Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993–1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:23:01 1998; MasPar time 29.42 Seconds
634.618 Million cell updates/sec

Tabular output not generated.

Title: >US-08-951-733-20
Description: (1-1154) from US08951733.pep
Perfect Score: 8624

Sequence: 1 HASGQRCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq32

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 11:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 39.946; Variance 185.025; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	BB	ID	Description	Pred. No.
1	134	1.6	509	_	P91060	Predicted amino acid	3.67e-01
2	117	1.4	386	22	W18664	Fragmented human NF-H	5.36e+00
ω	118	1.4	399	_	R23846	Prepro form of human	4.60e+00
4	118	1.4	399	29	W40193	Mouse OP-2 protein.	4.60e+00
υ	118	1.4	399	29	W44314	Mouse osteogenic prot	4.60e+00
o	118	1.4	399	16	R85759	mOP-2.	4.60e+00
7	118	1.4	399	10	R54938	Osteogenic protein mO	4.60e+00
æ	118	1.4	399	7	R33908	Mouse osteogenic prot	4.60e+00
9	118	1.4	399	9	R46744	Mouse osteogenic prot	4.60e+00
10	118	1.4	399	10	R50201	Murine OP-2.	4.60e+00
11	118	1.4	399	9	R47253	mOP2.	4.60e+00
12	118	1.4	399	19	W00239	Mouse osteogenic prot	4.60e+00
13	118	1.4	399	26	W36856	Full length sequence	4.60e+00
14	118	1.4	399	10	R57974	Murine OP-2.	4.60e+00
15	118	1.4	399	7	R33411	Murine pro-OP-2-PP.	4.60e+00
16	118	1.4	399	12	R51646	mOP2-PP prepro form m	4.60e+00
17	118	1.4	399	25	W23144	Bone morphogenic prot	4.60e+00
18	118	1.4	399	9	R47293	mOP2.	4.60e+00

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37 pspsptetessagttgasaprrptgpdatpe-dstpvllrpwgrrsrrpcpsttrpltns 95

Query Match 1.6%; Best Local Similarity 29.5%; Matches 31; Conservative

Score 134; DB 1; Length 509; Pred. No. 3.67e-01; 28; Mismatches 41; Indels 5;

5

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19
114	114	114	114	113	123	124	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	118	118
1.3	'n	1.3		1.3	1.4	1.4	1.4	1.4		1.4	٠	1.4	1.4	1.4	1.4	1.4	1.4	1.4			1.4	٠	1.4	1.4	1.4	1.4
763 2														402 1								N	N	N		9
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W31852	W31855	R33933	P70350	P60623	R28150	R33907	W16366	R50200	R85760	R50238	R57973	R51647	R46732	W00238	R33410	R44759	R47252	R47292	R27291	R54937	R60578	W44315	W36855	W40192	R50239	R27292
	Mycobacterium tubercu	n hOP2 full	encoded by	Sequence A encoded by	Sugar beet chitinase	Human osteogenic prot	hippocampa	Human OP-2.	hOP-2.	Human OP-2.	Human OP-2.			Human osteogenic prot		Human osteogenic prot	hOP2.			protei	Osteogenic protein OP	Human osteogenic prot	Full length sequence	Human OP-2 protein.		Murine osteogenic pro
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ALIGNMENTS

RESULT	
ಕ	P91060;
DT	12-APR-1990 (first entry)
ЭE	Predicted amino acid seqence of the infectious bovine rhinotracheitis
Œ	virus (IBRV) gIII polypeptide
KW	Infectious bovine rhinotracheitis virus; IBRV; gIII gene;
WW	<pre>gIII polypeptide; glycoprotein III; Bovine Herpesvirus type 1;</pre>
KΨ	IBRV(NG)dltkdlgIII; IBR disease vaccine;
KW	
စ္တ	Infectious bovine rhinotracheitis virus (IBRV)/Bovine Herpesvirus type 1
PN	EP-316658-A.
B	24-MAY-1989.
ΡF	02-NOV-1988; 118266.
PR	03-NOV-1987; US-116197.
PA	(BAYU) Baylor College med (NOVA-).
PI	Kit M, Kit S, Otsuka H;
DR	WPI; 89-15220/21.
1 5	1.5 1
PT	Infectious bovine rhinotrachettis virus
PT	 which does not produce any antigenic IBRV gIII
PT	polypeptide(s) as result of deletion and/or insertion in
PT	IBRV gill gene
Sd	Fig. 3; 4lpp; English.
റ്റ	RMM = 54,621 dalton. It has features in common with envelope
റ്റ	glycoproteins of other herpesviruses. The first 21 AAs are hydrophobic
റ്റ	with the exception of Arg at position 6. This sequence could correspond
ဌ	to a signal peptide for membrane insertion and may well be removed
င္ပ	during translation and transport. AAs at positions 481-498 are strongly
റ്റ	hydrophobic and have the characteristics of a membrane-spanning region.
റ്റ	The carboxy terminal 11 AAs have a basic charge and may function as a
င္ပ	cytoplasmic anchor sequence. Four potential glycosylation sites are
36	present in the region between the putative signal sequence and the
2 6	Ceciionio 500 AP.
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                                                                                                                                                                                                                                     of a sequence comprising fragments of the coding sequence of the human neurofilament subunit NF-H gene corresponding to nucleotides 1-1162 of the wild-type NF-H gene. This region contains GAGAG motifs. Frameshift mutants of the tau, ubiquitin, apolipoprotein E, microtubule-associated protein 2 (MAP-2), neurofilament subunit L, M and H and amyloid A4 genes are claimed. All these genes share a common GAGAN motif (N-A, G, C or T), which is the site of common GA dinucleotide deletion(s) that cause neurodegenerative disorders. Antigenic peptides used for the production of antibodies, and small nucleic acid sequences derived from frameshift mutants are used in the diagnosis, prevention and treatment of cancer and neurodegenerative diseases, e.g. Parkinson's disease, Alzheimer's disease, Down's supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's disease, multiple sclerosis, and other degenerative diseases such as cardiovascular disease and rheumatoid arthritis.
                                                                                                                                                 Matches
                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-1996; IB1106.
02-OCT-1995; GB-020080.
11-JAN-1996; US-029832.
11-JAN-1996; US-029832.
(ROYA-) ROYAL NETHERLANDS ACAD AF (ROYA-) UNIV ROTTERDAM ERASMUS.
(UYUT-) UNIV STATE UTRECHT.
Burbach JPH, Grosveld FG, Van I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Tby/yb.

Use of mutant genes having frame:shift mutation(s) - for developing prods. for the diagnosis, prevention and treatment of associated diseases, e.g. cancer or neuro:degenerative disease Claim 22; Fig 9; 123pp; English.

W18663 and W18664 are +2 and +1 frameshift mutations, respectively, w18663 and w18664 are respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUJ-1997 (first entry)
Fragmented human NF-H gene +1 frameshift mutant product.
Fragmented human NF-H gene +1 frameshift mutation; diagnosis;
Frameshift mutation product; GAGA motif; somatic mutation; diagnosis;
detection; antibody; probe; cancer; neoplasia; neurodegenerative;
Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;
Down's syndrome; frontal lobe dementia; progressive supraniclear palsy;
PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 97-226235/20.
N-PSDB; T69796.
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W18664;
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FCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRP
                               grgggpragalraggrggargpaeegagaaggvrlpaapppgrggra
                                                                       AGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRP-PRPW
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                                                                                                                                                                     Similarity
                                                                                                                                                   Conservative
                                                                                                                                                                                                                           disease
AA;
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production"
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                                                                                                                                             Score 117; DB 22;
Pred. No. 5.36e+00;
26; Mismatches 50;
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RESULT
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AC W4
DT 08
DE M6
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                           New osteogenic polypeptide(s) and their dimeric proteins - useful
y in association with a matrix for bone reconstitution after
orthopaedic and plastic surgery
Disclosure; 51-53; 69pp; English.
The sequence encodes the prepro form of human osteogenic polypeptide-2
(h0p2-pp). The protein is useful as a subunit of osteogenic and
proteins capable of endochondral bone formation, and allogenic and
xenogenic implants in mammals. When implanted with a matrix, the
polypeptide locally induces the full developmental cascade of
endochondral bone formation and bone marrow differentiation. This
can be used for optimal predictable bone formation to correct, eg
can be used for optimal predictable bone formation to correct
can be used for optimal predictable bone formation to correct anomalies, and to treat non-union fractures. The polypeptide also
has dental and periodontal applicns., and may be used for cartilage
                                          JLT 4
W40193 standard; Prot
W40193;
08-JUN-1998 (first e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09207073-A.
30-APR-1992.
18-OCT-1991;
18-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R23846
Mouse OP-2 protein.
Osteogenic protein; OP-2; bone morphogenic protein; OP/BMP chronic renal failure; renal therapeutic agent; disease; di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prepro form of human osteogenic polypeptide-2. Human osteogenic polypeptide-2; prepro sequence; implant; endochondral bone formation; skeletal abnormality; dental
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                    repair,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CREA-) CREATIVE BIOMOLECULES Kuberasampath T, Oppermann H, WPI; 92-167153/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-union fracture; cartilage repair; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1992
                                                                                                                                                                                      194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; N24522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    periodontal
                                                                                                                                253 SLP 255
                                                                                                                                                            67
                                                                                                                                                                                                                  12
                                                                                                                                                                                                      glalcalggggpglrppp-gc-pqrrlg-ardrdvq-reilavlglpgr-prprappaas
| :| ||:: : ||| ||: :| :|: :|:
                                                                                                                                                            rlp 69
                                                                                                                                                                                        GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                        standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 399
                                                                                                                                                                                                                                              h 1.4%;
Similarity 39.7%;
25; Conservative
                                                                                                                                                                                                                                                                                                                  eg
                                                                                                                                                                                                                                                                                                     in osteoarthritis 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U07635.
US-599543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label
267..3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
297..39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= cleavage site for signal peptide removal
257..261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label = cleavage site to form mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= truncated
                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mature protein 'hOP2-A'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved
                                                                         399
                                                                                                                                                                                                                                              Score
Pred.
13; M
                                                                                                                                                                                                                                                                                                                    treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INC.
Ozkaynak E, Rueger
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                            118;
No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein 'hOP2-R'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         six cysteine skeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein 'hOP2-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                             DB 1;
.60e+00;
                                                                                                                                                                                                                                                                                                                    See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cysteine skeleton
                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                    WO9105802
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abnormality;
                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                6,
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NR N-PSDB; V10348.

PT Treatment of chronic renal failure - using an osteogenic protein/bone morphogenetic protein renal therapeutic agent or protein/bone morphogenetic protein recells

PT morphogen or renal mesenchymal progenitor cells

PT morphogen or renal mesenchymal progenitor cells

CC This sequence represents the mouse osteogenic protein, OP-2. This sequence represents the mouse osteogenic protein daving, or at risk of, chronic renal failure which comprises administering an CC osteogenic protein/bone morphogenetic protein (OP/BMP) renal therapeutic agent or morphogen. The method can be used for treating e.g. chronic capent or morphogen. The method can be used for treating e.g. chronic conal failure, end-stage renal disease, chronic diabetic nephropathy, diabetic renal hypertrophy, hypertensive conditions of a content of a content or a batient or a batient
PRR 1111 PRR 11 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          """ repartsclerosis, hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary nephritis, renal dysplasia, or a patient afflicted with e.g. glomerular hypertrophy, tubular hypertrophy, glomerulosclerosis, tubulointerstitial sclerosis or renal fibrosis. Such therapeutic agents can prevent, inhibit or delay the progressive loss of functional nephron units and the progressive decline in glomerular filtration rate (GFR) which slowly but inevitably leads to the need for renal replacement therapy.
                                                                                                                              03-FEB-1998.
23-MAY-1995;
21-FEB-1992;
08-APR-1988;
15-AUG-1988;
23-FEB-1989;
17-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-1997;
06-MAY-1997;
06-MAY-1996;
                                                                           17-OCT-1989;
22-FEB-1990;
                                                                                                                                                                                                                                                                                                                          Mus sp.
US5714589-A.
                                                                                                                                                                                                                                                                                                                                                                            Mouse osteogenic protein OP2.
Mouse; osteogenic protein; subunit; endochondral bone formation; dimeric; recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W44314 standard;
W44314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1997; U07816.
06-MAY-1996; US-643321.
(CREA-) CREATIVE BIOMOLECULES
Cohen CM, Sampath KT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9741881-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nephropathy; glomerulopathy; hypertrophy; sclerosis; nephritis; mouse; dysplasia; fibrosis; glomerular filtration rate; GFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 LP 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 glalcalggghgprpp-htc-pqrrlg-arerrdmqreilavlglpgr-prpraqpaaar 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n CM, Sampath |
97-558690/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                   447570.

US-941646.

US-179406.

US-232630.

US-315342.

US-422613.

US-422699.

US-483913.

US-569920.

US-579865.
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18..263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- propeptide
264..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1..17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= 0p-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
12; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PT Extraction of osteogenic protein from mixture - using antibodies
PT specific for novel polypeptide chains useful as subunit(s) of
PT dimeric osteogenic protein(s)
PS Disclosure; Column 137-140; 127pp; English.

CC used in the present invention. The present invention describes methods
CC used in the present invention. The present invention describes methods
CC for selectively extracting an osteogenic protein (OP) from a mixture.
CC The method comprises: (a) exposing the mixture to an antibody that
CC specifically binds OP, separating the complex. In the methods OP
CC comprises a pair of oxidised subunits that are disulphide-bonded to form
CC a dimer, and one of the subunits has an amino acid (aa) sequence
CC sufficiently homologous to residues 335-431 of a 431 aa protein
CC designated OPS, sequence given in the specification. In dimeric form OP
CC capable of inducing cartilage and endochondral bone formation in a
CC mammal when disposed within a matrix implanted in the mammal. The
CC methods are used for recovering the recombinant proteins from cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-1990;
21-NOV-1990;
04-DEC-1990;
04-DEC-1990;
04-DEC-1991;
22-FEB-1991;
20-DEC-1991;
20-DEC-1991;
21-NOV-1993;
23-NAY-1993;
23-NAY-1995;
US5468845-A.
21-NOV-1995.
08-APR-1988;
08-APR-1988;
15-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R85759
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; osteogenic protein; hOP-1; murine; mOP-1; TGF-beta suftransforming growth factor-beta; dimer; antibody; epitope; hipurification; implantable osteogenic device; bone formation; anomaly; skeletal; dental; endochrondral bone formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1996 (first entry) mOP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 98-158353/14.
N-PSDB; V15217.
                                                                                                                                                    peptide
                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuberasampath
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                            non-union fracture; cartilage repair; osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254
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| :| ||:: :||| |: |:||| | : || ||||| : :|: :|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 1.4%;
Similarity 38.7%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRYKER CORP
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US-621849.
US-621988.
US-660160.
US-810560.
US-817052.
US-147023.
US-447570.
  179406.
US-179406.
US-232630.
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H,
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                                                                                                                                                      /note= "mOP-2
17..260
                                                                                                                                                                                                                                   claim
                                                                                                                                                                                                                                                                                   /note= "Prepro-peptide"
261..399
                                                                                                                                                                                                           303..399
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                        /note-
                                                                                                                              note-
                                                                                                                                                                                                                                   ហ្វ
                                                                                                                              "mOP-2 peptide,
                                                                                                                                                                                                                                                           "Mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H, Ozkaynak E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 29;
Pred. No. 4.60e+00;
12; Mismatches 22;
                                                                                                                                                                              peptide,
                                                                                                                                                                                                                                                           mOP-2, also designated
                                                                                                                                                                                 claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mOP-1; TGF-beta superfamily;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                             mOP2-Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                              hippocampus;
n; cranofacial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULTION ACCOUNTS TO THE SULTION ACCOUNTS TO THE SULT TO THE SULTION ACCOUNTS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies with osteogenic protein binding specificity - used in purification of osteogenic proteins, and as antigenic proteins Disclosure; Column 139-42; 129pp; English.

PS Disclosure; Column 139-42; 129pp; English.

CC This sequence represents the murine osteogenic protein, mop-2. mop-2 the mop-2 protein can be used in the TGF-beta superfamily. Fragments CC of tides which may be used in the generation of antibodies with CC peptides which may be used in the generation of antibodies are CC capable of binding specificities for osteogenic proteins. The antibodies are CC capable of binding specifically to an epitope of the osteogenic protein CC cand may be used in an implantable osteogenic device which allows predictable bone formation to correct acquired and congenital cC cranofacial and other skeletal or dental anomalies. They may be used to induce local endochrondral bone formation in non-union fractures and in cother clinical applications including dental and periodontal applications where bone formation is required. Other potential applications include cartilage repair, e.g. in the treatment of osteograrthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 24; Conser
                                                                                                                                                                                                                MUS SP.

WO9410203-A.

11-MAY-1994.

02-NOV-1993; U10520.

03-NOV-1992; US-971091.

03-NOV-1992; US-971091.

04-MAR-1993; US-029335.

31-MAR-1993; US-040510.
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17-CCT-1989
17-CCT-1989
22-FEB-1990
20-AUG-1990
07-SEP-1990
07-SEP-1990
07-SEP-1990
04-DEC-1990
04-DEC-1990
04-DEC-1990
22-FEB-1991
28-DEC-1991
28-DEC-1991
28-DEC-1991
28-DEC-1991
21-FEB-1993
01-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                    R54938 standard; Protein; 3
R54938;
15-OCT-1994 (first entry)
Osteogenic protein mOP2-P2-
                              A morphogenically active protein MOP-3 - morphogenesis in mammals
                                                                                                                                                              Cohen CM,
                                                                                                                                                                                                                                                                                                                                                                                                       Morphogenic protein; mOP-2-PP; OP-2; mOP-2; mOP-2; tissue morphogenesis; osteogenic protein.
                                                                                P-PSDB; Q65394
                                                                                                                                                                                             (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 96-010159/01.
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                                                                                                         n CM, Kuberasampath T, RHL, Rueger DC; 94-167392/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ф
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1989; US-315342
-1989; US-422699
-1989; US-422613
-1990; US-589920
-1990; US-579865
-1990; US-579865
-1990; US-518374
-1990; US-621849
-1990; US-621849
-1990; US-621849
-1990; US-621988
-1991; US-660162
-1991; US-860162
-1992; US-810560
-1992; US-810560
-1993; US-810560
-1993; US-816466
-1993; US-816466
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llarity 38.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oppermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399
  164pp; English
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Pred.
12; M
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                                                                                                                                                                 Oppermann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ozkaynak E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 re 118; DB 16; L
1. No. 4.60e+00;
Mismatches 22;
                                                                                                                                                                 H,
                                                       for inducing tissue
                                                                                                                                                              Ozkaynak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rueger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                              01-APR-1993.
28-AUG-1992; UO7432.
30-AUG-1991; US-752764.
30-AUG-1991; US-752857.
30-AUG-1991; US-752861.
31-UUI-1992; US-953780.
(CREAT) CREATIVE BIOMOLECULES INC.
COhen CM, Kuberasampath T, Oppermann H,
Pang RHL, Rueger DC, Smart JE;
Pang RHL, Rueger DC, Smart JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse osteogenic protein 2 (mOP-2).

Bone; loss; increase; fracture; post-menopausal; senile; osteoporosis; hyperparathyroidism; skeletal microstructure de chronic renal failure; kidney disease; osteomalacia, vitamin deficiency-induced osteopenia, osteoporosis; Paget's disease; bone mass; imbalance; resorption; formation; dialysis; calciu
                                                                                     results in bone fractures or other defects in skeletal microstructure. Such diseases include chronic renal failure and other kidney diseases, osteomalacia, vitamin D deficiency-induced osteopenia or osteoporosis, postmenopausal or senile osteoporosis, hyperparathyroidism and paget's disease. The methods can be used for protecting individuals at risk for loss of bone mass such as postmenopausal females, aged individuals and individuals undergoing postmenopausal females, aged individuals and individuals undergoing
                                                                                                                                                                                                          post-menopausal or senile osteoporosis, hyperparathyroidism el Disclosure; Page 122-123; 162pp; English.
The sequence is that of mouse osteogenic protein 2 (mOP-2) a a morphogenically active protein which may be used as part of method for treating a bone fracture or a disease which causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LT 8
R33908 standard; Protein; 399
R33908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A novel mouse morphogenic protein, OP3, has the sequence given in R54934, and is encoded by cDNA of sequence Q65390. cDNA and proteit sequences were also provided for human osteogenic protein OP1 (Q65391, R54935), mouse OP1 (Q65392, R54936), human OP2 (Q65393, R54937) and mouse OP2 (Q65394, R54938), as well as the genomic DNA sequence of human OP2 (Q65395). Generic sequences given in R54939 40 accommodate homologies between OP1, OP2, OP3 and other morphogen
                                                                    postmenopausal dialysis. The l
                                                                                                                                                                                                                                                                                                 pang RHL, Rueger DC, Smart JE;
WPI; 93-117208/14.
Use of morphogenic or in-vivo morphogenic-stimulating
prevent bone loss or increase, used for treating bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein family members.
                                    metabolism,
                                                    resorption or bone formation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9305751-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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                   induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 LP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 qp 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 1.4%;
Similarity 38.7%;
24; Conservative
                                                      The loss of bone mass may result from an imb
n or bone formation, an imbalance of calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolism; murine.
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genic protein 2
                                      a vitamin D imbalance or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "pro region, cleaved active protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "conserved seven cysteine skeleton"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cocation/Qualifiers
261..399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 118; DB 10;
Pred. No. 4.60e+00;
12; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                      Η,
                                                                                                                                                                                                                                                                                                                                                                      Ozkaynak
                                    nutritionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yield mature,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                          imbalance
                                                                                                                                                                                                                                                                                                 gagent - to fractures,
                                                      phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           defects;
                                                                                                                                                                                                                                                                                     etc.
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RESULT
A COLOR OF PET OF COLOR OF COLOR OF PET OF COLOR O
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PS Disclosure and Claims 25-26; Page 127-129; 160pp; English.
CC Murine osteogenic protein mOP2 and proteins having at least 70% CC homology with it are preferred morphogens for inclusion in new morphogen-enriched nutritional formulations. The formulations are dietary compositions suitable for people at risk for tissue CC damage due to protein energy malnutrition or to altered metabolism in function and infant formulations to enhance tissue development in CC an infant or juvenile.
       RESULT
ID R.
AC R.
DT 11
DE M.
KW 00
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KW 00
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Best Local S
Matches 2
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Best Local
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29-JUL-1993; U07190.
31-JUL-1992; US-923780.
31-JUL-1992; US-922813.
16-SEP-1992; US-946235.
04-MAR-1993; US-040510.
OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); 6NA(fx); BMP3(fx); BMP5(fx); BMP5(fx); GST-1(fx); GST-1(fx); MPF5(fx); MPF5(fx); GST-1(fx); MPF5(fx); MPF5(fx
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                                                                                                                                                                                                   Murine OP-2.
                                                                                                                                                                                                                                                                          R50201 standard;
R50201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CREA-) CREATIVE BIOMOLECULES INC. Jones WK, Kuberasampath T, Oppermann Rueger DC, Tucker RF, Cohen CM, Pang WPI; 94-065304/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse osteogenic protein mOP2. mouse osteogenic protein; mOP2; infant food formulation; tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R46744;
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                                                                                                                                                                                                                                   11-OCT-1994 (first entry)
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larity 38.7%;
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                                                                                                                                                                                                                                                                                                                  Protein;
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12; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118; DB 9;
No. 4.60e+00
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No. 4.60e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ozkaynak
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Best Local S
Matches 2
                                                                                                                               Jones WK, Kuberasampa
Rueger DC, Tucker RF;
WPI; 94-065689/08.
N-PSDB; Q56201.
Morphogenic protein soluble complex - for regeneration of the mammals and diagnosing tissue disorders (Claim 3; Page 75-77; 120pp; English. This sequence represents the murine derived protein, osteogrotein, mOp-2. The mature Op-2 protein was used as at protein, mOp-2. The mature Op-2 protein of the invention. dimeric protein subunit in the dimeric protein subunits which associated to give a structure with morphogenic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         effects of cancer therapy.

Claim 35-36; Page 115-117; ISipp; English.

Morphogens comprising an amino acid sequence sharing at least
Morphogens comprising an amino acid sequence sharing at least
70% homology with OP-1, OP-2, CBMP2, BMP3(fx), Vg1(fx), Vgr(fx),
DPP(fx), GDF-1(fx), 60A(fx) and at least 80% homology with
BMP5(fx) and BMP6(fx) are useful for maintaining the integrity of
the gastrointestinal tract luminal lining in a mammal, including
(1) limiting epithelial cell proliferation, (2) inhibiting ulcerative
lesion formation, (3) inhibiting inflammation normally associated
with ulcerative diseases, and/or (4) stimulating the repair of
ulcerative lesions and the regeneration of the luminal tissue.

Sequence 399 AA;
                                                                                                                                                                                                    17-FEB-1994.
29-JUL-1993;
31-JUL-1992;
31-MAR-1993;
31-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CREA-) CREATIVE BIOMOLECULES Charette MF, Cohen CM, Kuber Ozkaynak E, Pang RHL, Rueger WPI; 94-118121/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1994.
15-SEP-1993;
15-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                         R47253
R47253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maintaining integrity of gastrointestinal lining using a morphogen (stimulant) - for treating or preventing ulceration, also to inhibit endothelial cell proliferation and reduce side
                                                                                                                                                                                                                                                                                                                   Human; hippocampus; osteogenic protein; OP-1; subunit; dimer; morphogenic activity; cysteine; morphogen; family; pro-region; complex; soluble; aqueous solvent; therapeutic composition; symptom-alleviating; co-factor; antibody; diagnosis; assay;
                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                        quantitate;
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31-MAR-1993;
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WO9406420-A.
                                                                                                                                                                                           (CREA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                          CREATIVE BIOMOLECULES
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                                                                                                                                                                           Kuberasampath
                                                                                                                                                                                                                                                                                                        mature
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US-923780.
US-029335.
US-040510.
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llarity 38.7%;
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US-029335.
US-040510.
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Pred.
12; M
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No. 4.60e+00;
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                                                                                                                                                                            Ozkaynak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 399
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                                                                         osteogenic
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                       Mouse embryo full-length osteogenic protein OP-2 (W00239) includes a pro-sequence and the morphogenically active mature protein sequence (see also W00224) that includes a 7-Cys C-terminal domain. OP-2 can be expressed from intact or truncated cDNA (T33444) in prokaryotic or eukaryotic host cells. Mature Op-2 and other morphogens (see also W00221-35), partic. human OP-1 (W00221), can be used to induce dentine morphogenesis, to seal dental
                                                                                                                                                                                                                                                      cavities and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charette MF, Ruthe WPI; 96-412583/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 61-63; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tooth cavities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of morphogen(s), e.g. osteogenic proteins, on dentinalfor inducing dentine morphogenesis, desensitising teeth or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T33444
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01-MAR-1995; US-396
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                                                  194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                   Similarity
24; Conse
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llarity 38.7%;
Conservative
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                                                                                                                                                                                                                                                                                 to desensitise teeth to pressure and/or temp.
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18..260
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Pred. No. 4.60e+00;
12; Mismatches 2;
                                                                                                                                                                              Score 118;
Pred. No. 4
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                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a mouse osteogenic protein-2 (mOP-2).

CC OP-2 proteins are a group of morphogenically active proteins. Morphogens CC are inactive when reduced, but are active as oxidised homodimers and when CC oxidised with other morphogens (e.g. w36853-62). Comparison of the amino CC acid sequences of these morphogens has identified a consensus 6-7 CC cysteine motif at the C-terminal. Morphogenic proteins such as OP-2 play CC an important role, not only in embryogenesis, but also in tissue and CC organ maintenance and repair in mammals. They induce a developmental CC cascade of tissue-specific morphogenesis in a mammal. A novel method is CC described for screening a candidate compound for the ability to modulate cypression of a cellular gene encoding a naturally occurring morphogenic CC protein. The candidate compound is incubated with epithelial cells which CC express the cellular gene, and after a period of time the epithelial CC cells are assayed for the presence of or the amount of the protein CC expressed by the cellular gene. A change in the level of the morphogenic compounds of the compound that the opithelial colls in the amount of the protein CC expressed by the cellular gene.
                                                                                                                                                                                     Query Match
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                           expressed by the cellular gene. A change in the level of the morphogenic protein relative to the level in the epithelial cells in the absence of the candidate compound is indicative of the ability of the compound to modulate expression of the cellular gene. The method can be used to identify compounds which can increase or decrease morphogen production or levels. Such compounds can be used in the treatment of, e.g.arthritis, emphysema, osteoporosis, kidney disease, lung diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 13
W36856 standard; Prótein; 399
W36856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Full length sequence of mouse osteogenic protein 2 (hOP-2). Mouse osteogenic protein; OP; OP-2; morphogen; morphogenic prote embryogenesis; organ maintenance; tissue-specific morphogenesis;
                                                                                                                                                                                                                              cardiomyopathy, and cirrhosis Sequence 399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening for compounds which modulate morphogen expression incubating in the presence of epithelial cells which contain cellular gene for morphogenic protein expression Disclosure; Columns 67-70; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pang RH, Rueger DC, WPI; 97-384665/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1992; US-938021.
30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arthritis;
                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cohen CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5650276-A.
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 254 LP 255
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                                                                          194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                                    Local
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24; Conser
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M, Kuberasampath T, Oppe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     emphysema; osteoporosis; cirrhosis.
                                                                                                                                                1.4%;
larity 38.7%;
Conservative
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mature morphogenically
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                                                                                                                                                  Pred.
12; |
                                                                                                                                                                    Score 118;
Pred. No. 4
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                                                                                                                                                DB 26; 1
1.60e+00;
ches 22;
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R57974 standard; Protein; R57974;

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(first entry)

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RESULT 15
ID R33411 standard; Protein; 399 AA.
AC R33411;
DT 15-JUL-1993 (first entry)
DE Murine pro-Op-2-pp.
KW morphogenic; osteogenic protein; developmental cascade; mOP-2;
KW mouse; inflammation; anti-inflammatory; Transforming Growth Factory
KW TGF-beta super-family; hippocampus.
OS Mus.
FH Key Location of the control of the cont
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W09406399-A.
31-MAR-1994.
15-SEP-1993; U08742.
15-SEP-1992; US-945285.
15-SEP-1993; US-029335.
31-MAR-1993; US-040510.
(CREA-) CREATIVE BIOMOLECULES INC.
(CREA-) CREATIVE SIMOLECULES INC.
COPEN, Kuberasampath T, Oppermann H,
Pang RHL, Rueger DC, Smart JE;
WPI; 94-118107/14.
W09304692-A.

18-MAR-1993.
28-AUG-1992; U07358.
30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
30-AUG-1991; US-753059.
(CREA-) CREATIVE BIOMOLECULES INC.
COHEN CM, Kuberasampath T, Oppermann H, Pang RHL, Rueger DC, Smart JE;
WPI; 93-100652/12.
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Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, Vgl(fx), Vgr(fx), DPP(fx), GDF-1(fx), 60A(fx) and at least 80% homology with BMP3(fx), BMP5(fx) and BMP6(fx) are useful for integrating an implanted tooth in a tooth socket and for inhibiting tissue loss associated with periodontal disease or injury.
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CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP6(fx); GDF-1(fx); 60A(fx); BMP5(fx);                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tooth socket; alveolus; osteogenic protein; morphogen; morphogenic protein; periodontal tissue; regeneration;
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Local Similarity 38.7%;
ses 24; Conservative
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/note= "contains conserved 7 cysteine
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Pred. No. 4.60e+00;
12; Mismatches 22;
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Morphogen-induced modulation of inflammatory response - and morphogen-induced modulation of inflammatory response - and resulting tissue damage, e.g. in autoimmune diseases, diabetes, asthma, ischemia reperfusion injury, etc.

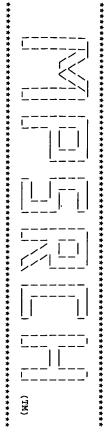
Claim 26; Page 126-127; 165pp; English.

Osteogenic protein (OP) -2 is a preferred morphogen for use in treating tissue damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes autoimmune disease, arthritis, psoriasis, dermatitis, diabetes achd sequences can also be used. See R33401 for mature mOP-2. Sequence 399 AA;
                                                                              194
  254 LP 255
                                     68 qp 69
                                                                                                 12 glalcalggghgprpp-htc-pqrrlg-arerrdmqreilavlglpgr-prpraqpaaar 67
                                                                                                                                                      / Match 1.4%;
Local Similarity 38.7%;
Local Similarity 38.7%;
les 24; Conservative
                                                                              GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                      Score 118; DB 7;
Pred. No. 4.60e+00;
12; Mismatches 22
                                                                                                                                                                                              Length 399
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:20:51 1998; MasPar time 40.56 Seconds 971.396 Million cell updates/sec

Tabular output not generated.

>US-08-951-733-20 (1-1154) from US08951733.pep 8624

Description: Perfect Score: Sequence:

1 HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 107076 seqs, 34141958 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 54.111; Variance 116.481; scale 0.465

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
314 162 153 136 136 136 137 137 137 129 129 129 129 129 121 121 127 127 127 127 127 127 127 127	Score
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S53396 QOBE3 QOBE3 QOBE3 PHUSD S16681 S019560 S11790 S110889 A28996 S27923 J00405 A280966 C29149 A60533 S00054 MMBE38	븀
hypothetical protein BHLF1 protein - human virion protein protein proline-rich protein salivary proline-rich homeotic protein - hu hypothetical protein - oRF4 protein - Orf vi proline-rich protein nodulation protein nodulation protein proline-rich protein proline-rich protein proline-rich protein proline-rich protein proline-rich protein testis-specific prote gene LF3 protein - hu hypothetical 119.5K p proline-rich protein odulation protein no epithelial tumor anti infected cell protein	Description
1.01e-30 1.01e-30 1.01e-00 1.02e-04 1.02e-04 1.02e-04 1.02e-04 1.02e-03 1.0	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	3 2	31	30	29	28	27	26	25	24
115	113	114	113	113	114	115	114	115	114	114	116	116	115	114	119	124	123	118	123	125	125
μ. ω	μ. ω	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.4	1.4	1.4	1.4	1.4	1.4	1.4
3149	1335	705	704	668	408	392	373	338	321	301	295	270	260	202	515	464	439	431	403	402	381
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BPLF1 protein - human	mucin precursor, panc	synapsin I splice for	synapsin Ia - rat	synapsin Ib - human	cyclin E - African cl	salivary proline-rich	hypothetical protein	HYA22 protein - human	nodulation protein no	proline-rich protein	proline-rich proteogl	miaE protein - Salmon	proline-rich protein	hypothetical protein	epithelial tumor anti	extensin - Volvox car	chitinase (EC 3.2.1.1	hypothetical protein	<pre>prpL2 protein - human</pre>	prepro osteogenic pro	hypothetical protein .
6.28e-01	1.05e+00	8.14e-01	1.05e+00	1.05e+00	8.14e-01	6.28e-01	8.14e-01	6.28e-01	8.14e-01	8.14e-01	4.83e-01	4.83e-01	6.28e-01	8.14e-01	2.18e-01	5.61e-02	7.38e-02	2.85e-01	7.38e-02	4.26e-02	4.26e-02

ALIGNMENTS

Qy 707 DI-HRAWRT	Db 501 QIADRI-KE	649 -	Db 444 KSNNEFRII	QY 590 FQKNRLFFY	Db 388 STVTIVYF-	Qy 530 LTWKMSVRE	Db 330 LLKKLRLKE	Qy 470 LVQLLRQHS	Db 271 LSHLSRQSF	Query Match Best Local Similarity 24.38 Matches 118; Conservative	SUMMARY #ler	#gene #gene SG	GENETICS	##experimenta	##residues	լլ Le_		#description Th		REFERENCE S5	ACCESSIONS S5		ALTERNATE_NAMES hy	TITLE hy	RESULT 1
DI-HRAWRTEVLRV-RA-QDPPPELYEVKVDVTGAYDTIPQ-DRLTEVIASIIKPQNTYC 762	QIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF 558		KSNNEFRIIAIPCRGADEEEFTIYKENHK-NA-IQPTQKILEYLRNKRPTSF-TKIYSPT 500	FQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHRE-ARPALLTSRLRFIPK 648	STVTIVYF-RHDTWNKLITPFIVEYFKTY-LVE-NNV-CRNHNSYTLSNFNHSKMRIIPK 443	: :: : : : : : :	LLKKLRLKDERWLEIS-DIWETKHNEENLNQLAIC-FISWLERQLIPKIIQTEFYCTEIS 387	LVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQE 529	LSHLSRQSPKER-VLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLLSLPLNGYLPFDS 329	3.6%; Score 314; DB 2; Length 884; arity 24.3%; Pred. No. 1.01e-30; Conservative 122; Mismatches 202; Indels 44; Gaps 37;	#length 884 #molecular-weight 102662 #checksum 7604	##CTOSS-Teferences SGD:S0004310; MIPS:YLR318w		##CIOSS-TETETETICES EMBLICATORO NED: 92220102, FED: 9002130, MIFG: IESSION ##experimental_source strain S288C (AB972)	84 ##label DUZ	ype DNA .	\$53396	The sequence of S. cerevisiae cosmid 8543.	Z	\$53390	53396	#formal_name Saccharomyces cerevisiae	cerevisiae) hypothetical protein L8543.12	S53396 #type complete hypothetical protein YLR318w - yeast (Saccharomyces	

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RESULT
ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #contents annotation; protein coding region
COMMENT The sequence contains four perfect repeats (residues 149-273,
274-398, 399-523, and 524-648).
CLASSIFICATION #superfamily human herpesvirus 4 BHLF1 protein
SUMMARY #length 660 #molecular-weight 66244 #checksum 8900
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#title
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##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 1.9%;
Local Similarity 30.8%;
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                                                                                                                                                                                                                                                                                        ASRSLPLPKRPRRGAAPEPER-TPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLE
                                                                                                                                                                                                                                                                                                                              TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPADPP--AAARLPPERQEPRLP 364
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                               v1rion type complete
v1rion TIF; BHY-1 protein homolog; ICP25; Vmw65; Vp16
alpha TIF; BHY-1 protein homolog; ICP25; Vmw65; Vp16
#formal_name bovine herpesvirus 1
05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S Satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, Nature (1984) 310:207-211

DNA sequence and expression of the B95-8 Epstein-Barr v
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09-Sep-1997
JC1306; S24229
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Sequence analysis of the 17,166 bp EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BHLF1 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-reb-1985 #sequence_revision 25-Feb-1985 #text_change
23-Aug-1997
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Pred. No. 6.63e-07;
34; Mismatches 60
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KEYWORDS DNA binding;
SUMMARY #length 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Ann, D.K.; Carlson, D.M.
#journal J. Biol. Chem. (1985) 260:15863-15872
#title The structure and organization of a p:
for a mouse multigene family.
#cross-references MUID:86059475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal #title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type DNA
##residues 1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##cross-references EMBL:Z11610; NID:g1065725; PID:e264419; PID:
This protein interacts with cellular transcription factors
transactivate immediate early viral genes.
                                                                                                                  317
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                                                                                                                                                                                     PRRGAAPE-PERTPYGQGSWAHPG-RTRGPSDRGFCVVSPARPAEEATSLEGA-LSGTRH
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                                                                                                                                   ppppGGPQPRPPQGPPPTGPQPRPTQGP-PP 172
: |: | | :: | | |: | | | : | ||
                                                                                                                                                                                                                         PQGPPPPGGPQQRP-PQGPPPPGGPQPRPPQGPPPPAGPQPRPPQGPPPPAGPHLRPTQG
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                                                                                                                                                                                                                                                                                                                                    h 1.6%;
Similarity 27.2%;
41; Conservative
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Similarity 31.3%;
46; Conservative
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Carpenter, D.E.; Misra, V.
Gene (1992) 119:259-263
Gene (1992) the bovine herpesvirus 1 homologue of
Sequences of the bovine herpesvirus 1 homologue of
simplex virus type-1 alpha-trans-inducing factor
                                                                                                                                                                                                                                                                                                                                                                                                             1-240 ##label ANN
#superfamily proline-rich protein
#length 240 #checksum 5152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B24264 #type fragment
proline-rich protein MP3 - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
09-Sep-1987 #sequence_revision 09-Sep-1987 #text_cl
03-May-1996
B38965 #type complete
hypothetical protein B (insertion
Enterobacter agglomerans
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Pred. No. 1.87e-03;
38; Mismatches 65;
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Pred. No. 1.12e-05;
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REFERENCE A92492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal Genetics (1988) 120:267-278
#title Length polymorphisms in human proline-rich
#cross-references MUID:89121440
#accession S03176
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Best Local Similarity 33.7%;
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                                                                    #cross-references MUID:85289325
#accession D25372
##molecule_type mRNA
##residues 1-36,'E',38-112,'T',114-115,'P',117-121,185-271,'A'
##residues 273-310 ##label MAE
                                                                                                                                                                                             644 RFIPKPDGLRPIVNMDYVVGA-RTFRREK 671
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##cross-references GB:X78052; NID:g459246; PID:g459248
# #length 276 #molecular-weight 31718 #chec
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                                                                                                   Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O. J. Biol. Chem. (1985) 260:11123-11130 Differential RNA splicing and post-translational cleavages the human saliyary proline-rich protein gene system:
                                                                                                                                                                                                                                                                                   S10890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       basic proline-rich protein IB-5; proline-rich peptide P #formal_name Homo sapiens #common_name man 19-Feb-1984 #sequence_revision 12-Apr-1996 #text_change
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03-Nov-1995 #sequence_revision 03-Nov-1995
09-Sep-1997
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S03176; S03175; S10890; D25372; E38355; A03295; A61294;
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Gene (1995) 156:37-42
IS1222: analysis and distribution of a new
in Enterobacter agglomerans 339.
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##residues 241-254,'KN',257-310 ##label KAU
  259
                                    221 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 280
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##residues 54-57,'E',59-73,'R';82-101 ##label
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es 40; Conservative
                                                                                               QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP
  RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
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FEBS Lett. (1996) 382:289-292

Tannin interactions with a full-length human salivary proline-rich protein display a stronger affinity than with
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J. Biochem. (1983) 93:495-502
Complete amino acid sequence of a
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Basic proline-rich proteins from human parotid relationships of the covalent structures of from a single individual.
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J. Biochem. (1983) 93:857-863
Amino acid sequences of glycopeptides obtained from basic proline-rich glycoprotein of human parotid saliva.
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241-252 ##label CHA
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    predicted
ith 310 #molecular-weight 31351 #checksum 3960
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41; Mismatches 52
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                                                                                                           ##residues 1-628 ##label |
##cross-references EMBL:X07441
                                                                                                                         ##molecule_type genomic RNA
##residues 1-628 ##label MOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 RAWNHSVREAGV-PLGLPAPGARRRGGSASRSLPLPKRPRRG-AAPEPERTPVGQGSWAH 280
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Similarity 30.9%;
21; Conservative
h 1.6%;
Similarity 25.0%;
73; Conservative
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                                                                                                                                                                                                                      Morch, M.D.; Boyer, J.C.; Haenni, A.L.
Nucleic Acids Res. (1988) 16:6157-6173
Overlapping open reading frames revealed by complete
nucleotide sequencing of turnip yellow mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deguchi, Y., Kehrl, J.H.
Nuclect Acids Res. (1991) 19:3742
Nucleotide sequence of a novel divenced a DNA binding protein.
                                                                                                                                                                           S01955
                                                                                                                                                                                                                                                                                                                               hypothetical protein, 69K - turnip yellow mosaic virus #formal_name turnip yellow mosaic virus, TYMV 21-Nov-1993 #sequence_revision 26-May-1995 #text_change
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#length 316
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Library, January 1991
erfamily unassigned homeobox proteins;
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Score 137; DB 2; Length 628
Pred. No. 1.40e-03;
64; Mismatches 134; Indels
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Pred. No. 1.87e-03;
20; Mismatches 24
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GPVLTETKPRTSVRQPRSATRGPSFRPILLPKV-VH-VHDDPPHSSLRPRGSRSRQLQPT

PID:g53182

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#journal Virology (1990) 176:379-389
#title Sequence analysis of the inverted terminal repetition in
#title genome of the parapoxvirus, orf virus.
#cross-references MUID:90266454
                                                                                   #journal Eur. J. Biochem. (1991) 202:969-974
#title Gene sequence of mouse B-type proline-rich protein MP4.
Transcriptional start point and an upstream phylogenetic footprint with ets-like and rel/NFKB-like elements.
#cross-references MUID:92111548
                                                                          #accession
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                                                                                                                                                                                                                                                                                                                                                                                                278 WAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                  209 RASSGPPRRSAARS-SAASGSRPAASGPAARAPAASSARTSAGEGAARGPGAPRAGW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 1-264 ##label FRA
##cross-references GB:M30023; EMBL:M37623; NID:g332561; PID:g332566
# #length 264 #molecular-weight 25613 #checksum 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 NHAQC-PYGYLLKTHCPLRA-AVTPAAGVCAREKPQGSVAAPEEEDTDPRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 SVLPRTSPRRGLLPNPRRHRTSTGHIPPTTTSRPTGPPSRLQRPVH-LYQSSPHTPNFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 VRRPLLAPNQFHSPRQPPPLSDDPGILGPRPLAPHSTRDPPPRPI-TPGPSN-THDLRPL 272
   ##residues 1-300 ##label
##cross-references GB:X58438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
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Similarity 28.2%;
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ORF4 protein - Orf virus
#formal_name Orf virus
23-Aug-1991 #sequence_re
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9560; S22570
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Pred. No. 1.39e-02;
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NID:g53181;
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                                                                                                                                                                                               R.; Bannister, A.J.;
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FERENCE $22570

Fauthors Roberts, S.G.E.; Layfield, R.; McDonald, C.J.

Roberts, S.G.E.; Layfield, R.; McDonald, C.J.

Roberts, S.G.E.; Layfield, R.; McDonald, C.J.

Roberts, S.G.E.; Layfield, R.; McDonald, C.J.

Roberts, S.G.E.; Layfield, R.; McDonald, C.J.

Roberts, McDonald, R.J.

Roberts, McDonald, R
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##cross-references EMBL:X61126
#FICATION #superfamily proline-rich protein .
# superfamily proline-rich protein .
# superfamily proline-rich protein .
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##residues 1-302 ##label DAV
      126
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                                                                                                                                                                                                                                                                                                                                                                                             y Match 1.5%;
Local Similarity 31.4%;
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                                                                                                                                                       IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
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                                                                                                                       AFRALVAQCLVCVPWDA-RPPPAAPSFRQVSCLKELVARVL-QRLCERGAKNVLAFGFAL
                                                                                                                                                                                                                                                                                                  LMIERNLTAAARSINLSQPAMSAAVRRL-RSYFRDEL-FTMRGREFVPTP-R-AEDLAPA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA-EEATSLEGALSGTRHSHPS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGNQQGPPPQGGPQQRPTQPGNQQGPPQQGG-PQAPPRPGNQQGPPPQGPQGPPRTGNQQ 245
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      126
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Similarity 25.2%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *superfamily regulatory protein lysR DNA binding; transcription regulation *length 302 *molecular-weight 34274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davis, E.O.; Johnston, A.W.B. Mol. Microbiol. (1990) 4:921-932
Mol. Microbiol. (1990) 4:921-932
Analysis of three nodD genes in Rhizobium leguminosarum biovar phaseoli; nodDl is preceded by nolE, a gene who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nodD3
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21-Nov-1993 #seguence_revision 13-Jan-19
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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protein nodD3 - Rhizobium
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Pred. No. 7.89e-03;
40; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                              Score 126; DB 2;
Pred. No. 3.23e-02;
28; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conceptual translation
                                                                                                                                                                                                                                                                                                                                                                    46;
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Best Local :
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#title
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#journal Genetics (1988) 120:267-278
#title Length polymorphisms in human proline-rich
generated by intragenic unequal crossing
#cross-references MUID:89121440
                                                                                                                                                                                                                                                                        #cross-references MUID:88273214 #accession A28996
                                                                                                       16-317
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                                                                                                                                                                                                                                                                                                                                                                             #authors
                                                                                                                                                                                                                      ##molecule_type DNA
##residues 1-317 ##label
##cross-references GB:M23236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GPPP-QGGNQSQG-PPPHPGKPEGPPP-QGG-NQSQGPPPRP-GKPE-GPPPPQGGNQSQG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 LSGTRHSHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 -NKPRGPPPHPGKPQGPPPQEGNKPQRP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 LPLPKRPRRGAAPEPERTPYGQGSWAHPGRTRGPSDRG-F-CVVSPARPAE-EATSLEGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -p-pprpgkpegpppqggnQsQgppprpgkpegpppqggnQsQgppprpgkpegspsQgg 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 1.5%;
Similarity 30.4%;
                 1.5%;
Similarity 26.4%;
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proline-rich protein - human
#formal_name Homo sapiens #common_name man
07-Oct-1994 #sequence_revision 26-May-1995
08-Sep-1997
                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. (1988) 263:10887-10893
Molecular evolution of the mouse proline-rich proteir multigene family. Insertion of a long interspersed
                                                                 #domain signal sequence #status predicted #label SIG\
#product proline-rich protein M14 #status predicted
#label MAT
#length 317 #molecular-weight 31719 #checksum 8454
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                                                                                                                                                                                                                                                                                                                                                                                                                                             proline-rich protein M14 precursor - mouse #formal_name Mus musculus #common_name house 30-Jun-1989 #sequence_revision 30-Jun-1989 #t
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#length 309 #molecular-weight 30
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Pred. No. 1.39e-02;
Score 132; DB 2;
Pred. No. 5.93e-03;
38; Mismatches 64
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GB:J03891; NID:g200535;
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В

37

SGSQPRPPVNGSQQGPPPPGGPQPRP-PQGPPPPGGPQPRPPQGPPPPGGPQPRP-PQGP 94

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ACCESSIONS
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                                                                                 Query Match 1.5%; Score 132; DB 2; Length 924 Best Local Similarity 28.2%; Pred. No. 5.93e-03; Matches 37; Conservative 33; Mismatches 52; Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Mazarakis, N.D.; Nelki, D.; Lyon, M.F.; Ruddy, S.; Evans,
E.P.; Freemont, P.; Dudley, K.
#journal Development (1991) 111:561-571
#title Isolation and characterisation of a testis-expressed developmentally regulated gene from the distal inversion of the mouse t-complex.
#cross-references MUID:91372153
#accession S22933
                                                                                                                                                                                                                                                                                         #accession
                                                                                                                                                                                                                                                                                                                                #description
                                                                                                                                                                                                                                                                                                                                                         #submission
206 ARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRRGAA 265
                                                                                                                                                                        ##residues 1-924 ##label PAR
##cross-references EMBL:M35547; NID:g330420; PID:g330421
# #length 924 #molecular-weight 94304 #checksum
                                                                                                                                                                                                                       ##residues
                                                                                                                                                                                                                                          ##molecule_type DNA
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##cross-references EMBL:X52128; NID:g54852; PID:g54853
## #length 566 #molecular-weight 61970 #checksum
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##residues: 1-566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 1.5%;
Local Similarity 35.7%;
hes 30; Conservative
                                        38 AAPRAPGPEPRTRLOPATPRRSGAADPADPVGHPAA-PRAPGPEPRTRLO-PATPRRSGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 VTRGAPLPPSPG-KGHLGGTPSSH 116
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                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, August 1990
Sequence and transcription of Raji Epstein-Barr virus DNA
spanning the B95-8 deletion region.
S27923
                                                                                                                                                                                                                                                                                                                                                                                                                                                      $2/923 #type complete

gene LF3 protein - human herpesvirus 4
#formal_name human herpesvirus 4, Epstein-Barr virus
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_chan
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  $22933 #type complete
testis-specific protein Bs13 - mouse
#formal_name Mus musculus #common_name house mouse
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                         Parker, B.D.; Bankler, A.; Satchwell, S.; Barrell, B.; Farrell, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0-Sep-1997
                                                                                                                                                                                                                                                                preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127; DB 2; Length 566; Pred. No. 2.44e-02; 19; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change
                                                                                      9;
                                                                                                                                                                            8997
                                                                                    Gaps
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 323 RQHHAGPPSTS 333
                                                    PEPERTPYGQGSWAHPGRIRGPSDRG-FCVVSPARP-AEEATSLEGALSGTRHSHP-SVG 322
                                                                     ADPA-DPVGHPA-A-P-RAPGPEPRTRLQPATPRRSGAADPADPVGHPAAPRAPGPEPRT
                          RLQPATPRRSG
                          162
                                                                                  151
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Search completed: Fri Dec 18 Job time : 112 secs. 18:22:43 1998

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:25:25 1998; MasPar time 30.89 Seconds 1002.720 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGQRCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

74019 segs, 26840295 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 55.898; Variance 96.260; scale 0.581

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	×
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
162 153 150 142 142 133 133 133 133 125 127 127 127 128 118 118 119 119 119 119 119 119	Score
11111111111111111111111111111111111111	Query Match
560 500 500 500 500 500 500 500 500 500	Length
	DB BG
YHLL EBV ATIN HYMBN PRPL HUMAN V70K.TUMAN V70K.TUMAN PRPJ MOUSE NOD1.RHISN BMBA MOUSE BMPB.HUMAN UC61.HCMAN MFHJ.HUMAN WEZ_HPV05 VZ2_HPV05 VZ2_HPV05 VZ2_HPV05 NOD1.RSVEB MIAE_SALTY Y091_NPV0P ND03_RHILO ND01_BRAIG MATD_NEUCR PRP1_HUMAN	IJ
HYPOTHETICAL BHLF1 PRO ALPHA TRANS-INDUCING P SALIVARY PROLINE-RICH SALIVARY PROLINE-RICH 69 KD PROTEIN. SALIVARY PROLINE-RICH PROLINE-RICH PROTEIN M NODULATION PROTEIN D TESTIS-SPECIFIC PROTEIN M NODULATION PROTEIN D BONE MORPHOGENETIC PRO BONE MORPHOGENETIC PRO BONE MORPHOGENETIC PRO HYPOTHETICAL PROTEIN D REGULATORY PROTEIN E2. HYPOTHETICAL GENE 1 PR TRNA-(MS [2] 10 [6] A) -HYD HYPOTHETICAL 29.3 KD P NODULATION PROTEIN D MATING TYPE PROTEIN D MATING TYPE PROTEIN A SALIVARY PROLINE-RICH	Description
1.47e-07 4.56e-07 4.56e-05 5.72e-06 5.72e-06 2.15e-04 4.31e-04 2.31e-04 2.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 3.32e-03 5.42e-02 5.42e-02 5.42e-03	Pred. No.

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01-APR-1993 (REL. 25, CREATED)

45	44	43	42	41	40	39	38	37	36	35	34	ω S	32	31	30	29	28	27	26	25	4.7
105	105	105	107	107	107	106	106	107	115	113	108	114	113	112	110	113	111	111	110	114	+T-t
1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.3	1.3	1.3	1.3	1.3	μ. ω	1.3	1.3	1.3	1.3	1.3	1.3	٠.
2774	890	863	529	494	318	285	233	174	3149	1255	706	705	704	633	628	514	509	498	408	408	400
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MAPA_RAT	ACO1_ECOLI	HIS2_NEUCR	DNB2_ADE05	MFH1_MOUSE	NODD_RHILT	YAFY_ECOLI	YFJR_ECOLI	BAR1_CHITE	TEGU_EBV	MUC1_HUMAN	SYN1_BOVIN	SYN1_HUMAN	SYN1_RAT	LA17_YEAST	V70K_TYMVC	VE2_HPV5B	VE2_HPV36	VE2_HPV08	CGE3_XENLA	CGE2_XENLA	CORPLANTA
MICROTUBULE-ASSOCIATED	ACONITATE HYDRATASE 1	PHOSPHORIBOSYL-AMP CYC	EARLY E2A DNA-BINDING	MESENCHYME FORK HEAD P	NODULATION PROTEIN D.	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL TRANSCRIP	BALBIANI RING PROTEIN	LARGE TEGUMENT PROTEIN	MUCIN 1 PRECURSOR (POL	SYNAPSINS IA AND IB.	SYNAPSINS IA AND IB (B	SYNAPSINS IA AND IB.	PROLINE-RICH PROTEIN L	69 KD PROTEIN.	REGULATORY PROTEIN E2.	REGULATORY PROTEIN E2.	REGULATORY PROTEIN E2.	G1/S-SPECIFIC CYCLIN E	G1/S-SPECIFIC CYCLIN E	OF/ O OF DOTE TO CECEEN D
1.76e+00	1.76e+00	1.76e+00	9.79e-01	9.79e-01	9.79e-01	1.31e+00	1.31e+00	9.79e-01	8.54e-02	1.59e-01	7.28e-01	1.17e-01	1.59e-01	2.17e-01	3.99e-01	1.59e-01	2.95e-01	2.95e-01	3.99e-01	1.17e-01	1.1/6 01

ALIGNMENTS

RESULT ID A AC P	Оy	8 8	8 8 B	ew Pew Pew Pew Pew Pew Pew Pew Pew Pew P	AC DOT	RESULT
LT 2 ATIN_HSVBP STANDARD; PRT; 504 AA. P30020;	365 ODLAAAQRC-PAGPPPTRSGA-AAQRTHR-RPPGCP 397	::		Query Match 1.9%; Score 162; DB 1; Length 660; Best Local Similarity 30.8%; Pred. No. 4.64e-09; Matches 48; Conservative 34; Mismatches 60; Indels 14; Gaps 12;	YHLL_EBV STANDARD; PRT; 660 AA. PO3181; 21-JUL-1986 (REL. 01, CREATED) 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 115-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 115-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 115-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 125-JUL-1998 (REL. 31, LOTAIN B95-8) (HUMAN HERPESVIRUS 4). PARTICLA BALFI PROFEIN. SEQUENCE FROM N.A. MEDLINE; 84270667. BARKIER A.T., BIGGIN M.D., DEININGER P.L., FARRELL P.J., GLESON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN C., TUFFNELL P.S., BARKIER B.G.; NATURE 310:207-211(1984). EMBL; V01555; -; NOT_ANNOTATED_CDS. PIR; A03742; OQBE3. HYPOTHETICAL PROTEIN; EARLY PROTEIN; REPEAT. DOMAIN 149 648 4 X 125 AA TANDEM REPEATS. REPEAT 274 398 2. REPEAT 399 523 3. REPEAT 399 523 3. REPEAT 399 523 3. REPEAT 524 648 4. SEQUENCE 660 AA; 66244 MW; 372F08C5 CRC32;	LT 1

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RESULPTION OF SECOND DESCRIPTION OF SECOND D
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                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE: 93012773.

CARPENTER D.E., MISRA V.;
GENE 119:259-263(1992).

-!- FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF :
EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).

-!- SIMILARITY: TO OTHER HERPESVIRUSES ALPHA TRANS-INDUCING EMBL; Z11610; E264419; -.
EMBL; Z11610; E264419; -.
PIR: S24229; S24229.
PIR: S24229; S24229.

TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING.
TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P10161; P02813;
01-MAR-1989 (REL. 10, C
01-OCT-1996 (REL. 34, I
01-OCT-1996 (REL. 34, I
SALIVARY PROLINE-RICH F
                                                                                           CHAIN
SEQUENCE
                                                                                                                                        REPEAT;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).
BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).
                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                       SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SM
GENETICS 120:255-265(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRPM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 93012995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIRIDAE; DS-DNA ENVELOPED
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                      ; x07704; E265547;
A03295; PIHUSD.
S03175; S03175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QHHAGPPSTSRPPRPWDTPCPPVYAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APAEAGGGWRRSGSTRTRGRAARSTTGRLQRPCCGPRRRAKC-CRATP-RQRLR--ARGE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPACGGPSRARGGRRRASPANP-FGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRHTS-GSGAFSQ-GRRPGRVCRLGWACKARSGPARGGPGPSPVRSGLGLSR-ARGSPGP 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERTPVGQGSWAHPGRTRGPSDR-GF-CVV-S-PARPAEEATSLEGALSGTRHSHPSVGR
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                                                                                                                                                                                                                                 P19999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 1.8%;
Similarity 31.3%;
46; Conservative
  Similarity 29.3% 43; Conservative
                                                                                                                                                              PAROTID GLAND;
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83186122.
                                                                                   165
234 /
                                                                                                                                                                                                                                   1CTG
                                                                                             AA;
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                   1.7%;
                                                                                           234
23676 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
PROTEIN PO (ALLELE M) (CONTAINS: PEPTIDE P-D)
                                                                                                                                                              SALIVA; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                  SANADA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITHIES
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Pred. No. 1.47e-07;
33; Mismatches 56
Score 150; DB 1;
Pred. No. 4.56e-07;
41; Mismatches 53
                                                                                        PEPTIDE P-D.
ED2D4ADC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERTEBRATA;
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                                                                                             CRC32;
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  53;
                                           Length 234;
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Indels
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  10;
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Best Local S
Matches 4
                                                                      V70K_TYMV STAN

P10357;

01-MAR-1989 (REL. 1

01-AUG-1992 (REL. 2

01-AUG-1992 (REL. 2

69 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
CHAIN
SEQUENCE
TURNIP YELLOW MOSAIC VIRUS. VIRIDAE; SS-RNA NONENVELOPE [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRB4.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRPL_HUMAN STANDARD; PRT; 276 AA.
p10162; P02813;
01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SMI'
GENETICS 120:255-265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X07715; E4806; PIR; A03295; PIHUSD. PIR; S03176; S03176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 207-276.
MEDLINE; 83186122.
SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPPP-GKPER-PPPQGGNQSQG-P-PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPPP-QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPPP-GKPER-PPPPQGGNQSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGTRHSHPSVGRQHHAGPPSTSRPPRP
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                                                                                                                                                                                                                                                                                                        SHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                 APPAGKPQGPPPPPQGGRPPRP 268
                                                                                                                                                                                                                                                                                                                                                                                                     RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -P-PPHPGKPEGPPPQEGNKSRSARSPPGKPQGPPPQQEGNKPQGPPPPGKPQGPPPPGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P19999;
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40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAROTID GLAND; SALIVA; MULTIGENE FAMILY
                       SS-RNA NONENVELOPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%;
larity 28.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1CLG
                                                                                                                                                                                                     STANDARD;
                                                                                             10, CREATED)
23, LAST SEQUENCE UPDATE)
23, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMITHIES
                                                                                                                                                                                                                                                                                                        338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 142; DB 1; L
Pred. No. 8.72e-06;
41; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE P-D.
4838945A CRC32;
                            VIRUSES; TYMOVIRIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.;
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                                                                                                                                                                                                     628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 276;
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FREE COLORS REAL STREET FOR STREE
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Query Match
Best Local S
Matches 4
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Best Local
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                                                                                             REPEAT; PAROTID GLAND; MULT
SIGNAL 1 16
CHAIN 17 39
CHAIN 17 17
CONFLICT 37 57
CONFLICT 37 57
CONFLICT 218 218
SEQUENCE 247 AA; 25108 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRP4_HUMAN STANDARD,
p10163; P02813;
21-JUL-1986 (REL. 01, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANDITATION UPDATE)
01-OCT-1994 (REL. 30, LAST ANDITATION UPDATE)
                                                                                                                                                                                                                                                                                                           MEDLINE; 89121440.

LYONS K.M., STEIN J.H., SMITHIES

GENETICS 120:267-278(1988).

EMBL; K03207; G190508; -.

EMBL; X07882; G296670; -.

HSSP; P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: TO 65 TO 70 KD PROTEIN EMBL; X07441; G62223; ALT_SEQ. PDIR; S01955; S01955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE; 88289359.
MORCH M.D., BOYER J.C., HAENNI A.L.;
NUCLEIC ACIDS RES. 16:6157-6173(1988).
-!- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 89121440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 85289325.
MAEDA N., KIM H.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 Match 1.6%;
Local Similarity 25.0%;
les 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDA N., KIM H.-S., AZEN E.A., SMITHIES BIOL. CHEM. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASRSLPLPKRPRRGAAPEPERTPYG-QGSWA-HPGRTRGPSDRGFCVVSPARPAEEATSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHAQC-PYGVLLKTHCPLRA-AVTPAAGVCAREKPQGSVAAPEEEDTDPRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYRHRRPYPLLPNPPAALPSIAYTSSRGKIHHSLPKGALPK-EGAPPPPRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSIRKDALLQTGPRLGHLERLGQPANLRTSERSPPTKRRLPRSSEPNRLPKPLPEATLAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRRPLLAPNQFHSPRQPPPLSDDPGILGPRPLAPHSTRDPPPRPI-TPGPSN-THDLRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPPLYQLGAATQARPPPHAS-GPR-RRLGCERAWNHSVREAGVPLGLPAPGAR-RR-GGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPVLTETKPRTSVRQPRSATRGPSFRPILLPKV-VH-VHDDPPHSSLRPRGSRSRQLQPT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFLL-SSL-R--PSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EG-ALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLY-SSGDKEQLRP
  Similarity
40; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIMATES.
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  Conservative
                      1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69195 MW;
                                                                                                                                                                                                                                          MULTIGENE FAMILY; SALIVA; GLYCOPROTEIN;
                                                                                                  ₹
                                                                                        PROTEIN N1.

GLYCOSYLATED PROTEIN &
MISSING (IN REF. 2).

D -> A (IN REF. 2).

C -> B CRC32;
  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 137; DB 1; Let Pred. No. 5.26e-05; 64; Mismatches 134;
                         Score 133; DB 1;
Pred. No. 2.15e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9E64ED49 CRC32;
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  Mismatches
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  Indels
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                                                  247;
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  10;
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                                                                                                                                                                                                                                            SIGNAL
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  Gaps
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RESULT PRESULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                           NOD3_RHILP STAN
P23720;
01-NOV-1991 (REL. 2
01-NOV-1991 (REL. 2
01-NOV-1995 (REL. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987
13-AUG-1987
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE;
MEDLINE; 91014692.

DAVIS E.O., JOHNSTON A.W.B.;

MOL. MICROBIOL. 4:921-932(1990).

HOL. FUNCTION: NODD REGULATES THE E

WHICH ENCODE OTHER NODULATION

REGULATOR OF ITS OWN EXPRESSIO
                                                                                                                                 SEQUENCE FROM STRAIN-8002;
                                                                                                                                                                                                                   PLASMID SYM. PROKARYOTA; GRACILICUTES;
                                                                                                                                                                                                                                                                                       NODULATION NODD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:15863-15872(1985).
EMBL; M12100; G200549; -.
HSSP; P19999; ICLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUS MUSCULUS (MOUSE)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRP3_MOUSE P05143;
                                                                                                                                                                                                   RHIZOBIACEAE
                                                                                                                                                                                                                                                                RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROLINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT; SALIVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 HPSVGRQHHAGPPSTSRPPRPWDTPCPP 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATQARPPPHAS--GPRRRLGCE-RAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGPQPRPPQGPPPPAGPQPRPPQGPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PPHPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPBGKPQGPPPAGGNP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPRRGAAPEPERTPYGQGSWAHPGRTRGPSDRGFCVVSPAR-PAEEATSLEGALSGTRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPGGPQPRPPQGPPPPGG-PQPRPPQGPPPPGGPQQRPPQGPPPPGGPQQRPPQGPPPP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OQPODPPAGKPOGPPPPPOGGRPPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 39; Conser
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86059475.
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7 (REL. 05,
1 (REL. 30,
12H PROTEIN 1
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llarity 26.4%;
Conservative
                                                                                                                                                        N.A
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                                                                                                                                                                                                                                                                                                       . 20, CREATED)
. 20, LAST SEQUENCE UPI
. 32, LAST ANNOTATION U
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05,
05,
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5, LAST SEQUENCE UPI
0, LAST ANNOTATION (
N MP-3 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29521
    EXPRESSION.
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                                                                                                                                                                                                                       SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 131; DB 1;
Pred. No. 4.31e-04;
38; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                      EXPRESSION OF THE NOD ABCFE GENES N PROTEINS. NODD IS ALSO A NEGATIVE
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    BINDS
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    FLAVONOIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
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                                                                                                                                                                                                                         RODS
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Q01755;
Q1-NOV-1995 (REL. 32, CREATED)
Q1-NOV-1995 (REL. 32, LAST SEQUENCE UP
Q1-NOV-1997 (REL. 35, LAST ANNOTATION
TESTIS-SPECIFIC PROTEIN PBS13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X54215; G4623
PIR; S11790; S11790
                                                                                                                                                                                                                                                                       DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAZARAKIS N.D., NELKI D., LYON M.F., FREEMONT P., DUDLEY K.; DEVELOPMENT 111:561-571(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: TESTIS.
-!- DEVELOPMENTAL STAGE: FIRSTLY EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: POSSIBLY PLAYS AN IMPORTANT AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPRESSOR; PLASMID.
DNA_BIND 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 91372153
                                                                                                                                                                                                                                                                                                                                                                                                                 TESTIS;
                     239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: SOME TO YEAST L; X52128; G54853; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPERMATOCYTE STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMIERNLTAAARSINLSQPAMSAAVRRL-RSYFRDEL-FTMRGREEVPTP-R-AEDLAPA 72
                     PAPGARRRGGSASRSLPL-PKRPRRGAAPEPERTPVGQGS-WAHP-GRTRGPSDRG-FCV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFRALVAQCLVCVPWDA-RPPPAAPSFRQVSCLKELVARVL-QRLCERGAKNVLAFGFAL
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Similarity 31.4%;
38; Conservative
                                                                                                               Similarity
30; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                 SPERMATOGENESIS;
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                                                                                                             1.5%;
larity 35.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G46237; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TCP11.
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34274 MW;
                                                                                                                                                                                                     61970 MW;
                                                                                                                                                                                                                                                                          S; REPEAT; COILED COIL (5 HEPTADS).
COILED COIL (8 HEPTADS).
COILED COIL (2 HEPTADS).
COILED COIL (10 HEPTADS).
COILED COIL (10 HEPTADS).
                                                                                                          Score 127; !
Pred. No. 1.!
19; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126; DB 1;
Pred. No. 2.37e-03;
28; Mismatches 46
                                                                                                                                                                                                                                                  LEUCINE-RICH
LRR 1.
LRR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H-T-H MOTIF (BY SIMILARITY).; ED62D2FA CRC32;
                                                                                                                                                                                                     LRR 3.
7A421F03 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOK1
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                                                                                                               Mismatches
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                                                                                                                                DB 1;
.69e-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                               30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPERM DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                               <u>ن</u>
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Best Local S
Matches 4
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P05142;
P05142;
13-AUG-1987
13-AUG-1987
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOD1_RHISN P55359;
                                        EMBL; AE000065; G2182301; PROSITE; PS00044; HTH_LYSINODULATION; TRANSCRIPTION
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQ
01-NOV-1997 (REL. 35, LAST ANN
NODULATION PROTEIN D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                         PLASMID SYM PNGR234A.
PROKARYOTA; GRACILICU
                                                                                                                                                                                                                                                                                                                                                                                                                                    RHIZOBIUM SP. (STRAIN NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NODD1 OR Y4AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROLINE-RICH
                     REPRESSOR;
                                                                                                                                                                                                                                                                                                                                                                    RHIZOBIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 VSPARPAEEATSLEGALSGTRHSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 VTRGAPLPPSPG-KGHLGGTPSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19999; LUE
SALIVA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
40; Conserv
MULTIGENE
23 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 AA;
                                                                                                                                                                                                                                                                                                                                                                                         GRACILICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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26034
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27.08;
  E FAMILY;
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PERRET X.;

NATURE 387:394-401(1997).

NATURE 387:394-401(1997).

IF FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCFE GENES WHICH ENCODE OTHER NODULATION PROTEINS. NODD IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS.

IS SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE; 86059475.

ANN D.K., CARLSON D.M.;

AND D.K., CHEM. 260:15863-15872(1985)

EMBL; M12099; G200547; -.

HSSP; P19999; ICLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 VGRQHHA--GPPSTSRP-PRPWDTPCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 PPPPGGPQLRPPQGPPPPAGP-QPRPPQGPPPPAGPQPRPPQGPPTTGPQPRPTQGPPPT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 GGPQQQPPQGPPPPGGPQPRPPQGPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 PPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQQRPPQGPPPPGGPQPRPPQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAPE-PE-RTPYGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REL. 05, CREATED)
(REL. 05, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
H PROTEIN MP-2 PRECURSOR.
                                     D0044; HTH_LYSR_FAMILY; 1.
TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVATOR.
                                                                                                                                                                                                                                                        BAIROCH A., BROUGHTON W.J.,
                                                                                                                                                                                                                                                                                                                                                                SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 125;
Pred. No. 3.
33; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE UPDATE)
PLASMID.
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PROLINE-RICH PROTEIN
PD830DAF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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    MOTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
.32e-03;
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  (BY SIMILARITY).
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                                                                                                                                                                                                                                                          ROSENTHAL A.,
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Matches
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                                                                                                                                                                                                                                                                                      SIGNAL;
SIGNAL
PROPEP
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CARBOHYD
                                                                                                                                                                                                                             CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                  EMBL; M97017; G200141; -.
                                                                                                                                                                                                                                                                                                                                                                                             OEZKAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M., WARREN F.D., DRIER E.A., OPPERMANN H.;
J. BIOL. CHEM. 267:25220-25227(1922).
J. BIOL. CHEM. 267:25220-25227(1922).
J. BIOL. CHEM. 267:25220-25227(1922).
J. BIOL. CHEM. 267:2520-25227(1922).
J. BIOL. CHEM. 267:2520-25227(1922).
J. BIOL. CHEM. 267:2520-25227(1922).
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION AND BOURE HOMODIMER, DISULFIDE-LINKED.
J. SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
J. SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
J. SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2) (OP-2).
BMP8A OR BMP8 OR BMP-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BONE MORPHOGENETIC PROTEIN 8A PRECURSOR (BMP-8A) (OSTEOGENIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P34821;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM8A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
BMP8_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101
                                               254
                                                                                              194
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                                                                      8
                                                                                                                   12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUSCULUS (MOUSE).
MUSCULUS (MOUSE).
ARYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
             13
                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
                                                                     QP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVSCLKELVARV-LQRLCERGAKNVLAFGFALL
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                                                                                                                                                                                                                                                                                                                                     MGI:104515; BMP8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDA-RPPPAAPSFR 94
                                                                                              GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
28; Conser
                                                255
                                                                                                                                            Similarity
24; Conse
                                                                                                                                                                                                                                                                                                                GROWTH
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261
298
298
327
331
363
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larity 38.7%;
Conservative
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 STANDARD;
                                                                                                                                                                                                                                                                                                               FACTOR;
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                                                                                                                                                                                                                                                                                                                         TGF_BETA;
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399
396
396
398
155
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                                                                                                                                            Pred.
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Pred. No. 1.25e-02;
                                                                                                                                                                    Score
                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                             BONE MORPHOGENETIC PROTEIN 8A.
                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                              INTERCHAIN (BY SIMILARITY).
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 PRT;
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                                                                                                                                                                                          7075A1ED CRC32;
                                                                                                                                                                                                                                                                                                               BONE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                              Mismatches
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No. 3.
 402
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                                                                                                                                                       DB 1;
.30e-02
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Best Local S
Matches 2
                                                                                                                                                        01-AUG-1990
01-AUG-1990
01-FEB-1991
          SEQUENCE FROM N.A.

MEDLINE; 90269039.

CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,
HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A.,
PREDDIE E., SATCHWELL S.C., TOMLINSON P., WESTON K.M., BARRELL B.C
CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).

EMBL; X14403; E27260; -.

EMBL; X14403; E27260; -.
                                                                                                                                                                                        UL61_HCMVA
P16818;
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID DISULFID DISULFID DISULFID CARBOHYD CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OEZKAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.
WARREN F.D., DRIER E.A., OPPERMANN H.;
J. BIOL. CHEM. 267:25220-25227(1992).

-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY B
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGU
AND BONE HOMEOSTASIS (BY SIMILARITY).

-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
EMBL, M97016; G189390; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P34820;
01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
BONE MORPHOGENETIC PROTEIN 8 PRECURSOR (BMP-8)
                                                                                                                                    UL61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
CHAIN
                                                                                                             HUMAN CYTOMEGALOVIRUS (STI
VIRIDAE; DS-DNA ENVELOPED
                                                                                                                                               HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-HIPPOCAMPUS;
MEDLINE; 93094231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
EUKARYOTA; METAZOA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A45056; A45056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                           194
                                                                                                                                                                                                                                                 253 SLP
                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                      68 RLP 70
                                                                                                                                                                                                                                                                                           GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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                                                                                                                                                                                                                                                                                                                                       Similarity 39.7%;
25; Conservative
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                                                                                                                                                        (REL.
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S09824.
PROTEIN.
                                                                                                                                               PROTEIN UL61.
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15,
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39.7%;
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402
367
401
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                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                        (STRAIN AD169).
DPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOKINE;
                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                       Score 125; DB 1;
Pred. No. 3.32e-03;
12; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BONE MORPHOGENETIC I
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                     8F20C81B CRC32;
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                                                                                                                                                          UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                             Length 402;
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                                             B.G.;
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Search completed: Fri Dec 18 18:26:40 1998 Job time: 75 secs.
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Best Local Similarity 28.4%;
Matches 27; Conservative
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Best Local Similarity 32.1%;
Matches 27; Conservative
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SEQUENCE
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Q99958;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
MESENCHYME FORK HEAD PROTEIN 1 (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKH-14).
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PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKHL14 OR MEH1.
HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION
                                                                                                                         427 NHSGDLNHL-PGHTFAAQQQTFPNVREMFNSHRLG 460
                                                                                                                                                                                                                              367 SPLSALNLAAGQEGALAATGHHHQHHGHHHPQAPPPPPAPQPQPTPQPGAAAAQAASWYL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 YSSGDKEQLRPSTLLSSLRPSLTGARRLVETIFLG 389
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                                                                                                                                                                                                      SPARPAEEATSLEGALSGTRHSHPSVGRQH-HAGPPSTSRPPRPWDTPCPPVYAETKHFL 354
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163
387
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501 AA;
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167 Pp
396 H.
421 Al
408 Po
422 Po
422 Po
53719 MW;
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                                                                                                                                                                                                                                                                                                     Score 125; DB 1; Length 501; Pred. No. 3.32e-03; 28; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       FORK HEAD.

POLY ARG.

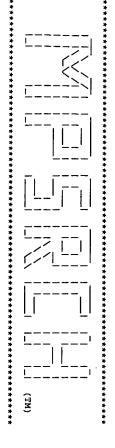
HIS-RICH.

ALA/PRO-RICH.

POLY-PRO.

POLY-ALA.

90D32EFA CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:27:02 1998; MasPar time 60.80 Seconds
945.090 Million cell updates/sec

Tabular output not generated.

Title: >US-08-951-733-20
Description: (1-1154) from US08951733.pep
Perfect Score: 8624

Sequence: 1 HASGORCVLLRTWEALAPAT.....TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptrembl6

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 54.168; Variance 101.474; scale 0.534

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result
110 110 110 1110 1110 1110 1110 1110 1	i se t
8465 8459 5161 6781 681 423 423 424 147 147 149 149 149 149 149 149 149 149 149 149	Score
98.2 598.2 7.998.1 1.1.6667.9 1.5568.2	Query Match
1132 1132 1132 1132 1132 988 989 1031 67 884 296 276 276 277 277 278 278 278 278 278 278 278 278	Query Match Length DB
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	BB
014746 014783 0704783 070372 013339 013338 0013338 005432 006163 0369118 0369118 0369118 036927 000600 046612 0946612 0946613 0946613 0946613 0946613 0946613 0946613 0946613 0946613 0946613 0946613	ID
TELOMERASE REVERSE TRA TELOMERASE SUBUNIT P12 TELOMERASE CATALYTIC S CHROMOSOME XII COSNID HYPOTHETICAL PROTEIN (WISKOTT ALDRICH SYNDRO PAROTID 'O' PROTEIN (FRA PROTED SYNTHASE (F IS 1222 GENE ORF A AND HOMEOBOX PROTEIN (FRA PROTEDE SYNTHASE (F HYPOTHETICAL 60.2 KD P PLENTY-OF-PROLINES-101 HOMOLOGUE OF RETROVIRA PROLINE RICH PROTEIN SALIVARY PROLINE-RICH PROLINE RICH PROTEIN	Description
0.00e+00 0.00e+00 0.00e+00 0.00e+010 1.37e-111 1.97e-60 2.25e-57 1.71e-35 7.18e-06 2.85e-05 4.02e-05 3.03e-04 7.93e-04 3.01e-03 3.01e-03 1.57e-03	Pred. No.

	44 115 1.3	115 1		115 1									118						117 1	126 1		132 1	133 1	128 1
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004528	000599	Q16038	Q07611	Q64306	041981	060585	022835	Q85027	043516	Q15220	Q41645	Q42421	052256	068033	Q53180	Q85028	Q62107	P91497	Q17626	Q65553	006264	Q99307	002123	Q53913
SEQUENCE OF BAC F20P5	CON1.	PRB1M PROTEIN (FRAGMEN	PROLINE-RICH PROTEOGLY	PROLINE-RICH PROTEIN.	HYPOTHETICAL 9.9 KD PR	SER/ARG-RELATED NUCLEA	SF16 ISOLOG.	VIRAL PROTEINASE.	WASP INTERACTING PROTE	PRPL-2 PROTEIN.	EXTENSIN (FRAGMENT).	CHITINASE PRECURSOR.	FLHF.	EXONUCLEASE SBCD HOMOL	MPIK3030 NODD1 GENE IN	SUBSTRATE OF THE PROTE	PROLINE-RICH SALIVARY	CODED FOR BY C. ELEGAN	C04G2.8.	UL36.	HYPOTHETICAL 131.9 KD	LF3 PROTEIN.	SIMILARITY TO COLLAGEN	BETA-KETOACYL SYNTHASE
1.72e-01	2.32e-01	2.32e-01	1.72e-01	2.32e-01	2.32e-01	1.48e-02	2.76e-02	9.42e-02	1.08e-02	2.02e-02	1.48e-02	2.02e-02	9.42e-02	9.42e-02	9.42e-02	9.42e-02	1.08e-02	9.42e-02	1.27e-01	7.85e-03	2.18e-03	1.14e-03	8.18e-04	4.15e-03

ALIGNMENTS

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241 GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG 300	203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262	181 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240	143 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 202	121 SYLPNTYTDALRGSGAWGLILLRRYGDDYLVHLLARCALFYLVAPSCAYQYCGPPLYQLGA 180	83 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 142	61 DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR 120	23 MPRAPRCRAVRSLLRSHYREVLPLATEVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 82	1 MPRAPRCRAVRSILRSHYREVLPLATFVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60	Query Match 98.2%; Score 8465; DB 4; Length 1132; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 1132 AA; 126995 MW; 2DFBEDF3 CRC32;	RNA-DIRECTED DNA POLYMERASE.	SCIENCE 277:955-959(1997).		NAKAMURA T.M., MORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,	MEDLINE: 97400623.	SEQUENCE FROM N.A.		EUTHERIA; PRIMATES.			REVERSE TRANSCRIPTASE	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)	(TREMBLREL. 05,	014746 PRELIMINARY; PRT; 1132 AA.	3

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01-JAN-1998
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SEQUENCE;
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EUKARYOTA;
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                    SAPIENS (HUMAN).
RYOTA; METAZOA; CHORDATA;
ERIA; PRIMATES.
                                                                                                                                                                                                                         LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLKVRAQDPPPELYFVKVDVTGAYDTI
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                                                                                                                     KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD
                                                                                                                                                FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
                                                                                                                                                                   NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLP
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                                                                                                                                         FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL
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98 (TREMBLREL. 05, L
98 (TREMBLREL. 06, L
E CATALYTIC SUBUNIT.
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                                                     LAST SEQ
                            VERTEBRATA;
                                                                                   PRT;
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ANNOTATION UPDAT
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                            TETRAPODA;
                                                       UPDATE)
                            MAMMALIA;
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EMBL; AF018167; G2347129; ...
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ONCOGENE 0:0-0(1998).
EMBL; AF051911; G3005592; -.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 1122 AA; 127977
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA
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                                   LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.; SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS EMBL; AF015783; G2340168; -.
EMBL; AL022299; EL285360; -.
PFAM; PF00078; rvt.
                                                                                                                                   STRAIN-972H-;
                                                                                                                                                                                         MEDLINE; 97400623.

NAKAMURA T.M., MORIN G.B., CHALINGNER J., HARLEY C.B., CECH SCIENCE 277:955-959(1997).
                                                                                                                                                                                                                                                                    STRAIN-972H-
                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                            EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                SCHIZOSACCHAROMYCES POMBE
 RNA-DIRECTED DNA POLYMERASE SEQUENCE 988 AA; 116328 I
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1057
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                                                                                                                                                                                                                                                                                                                              ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                              (FISSION YEAST).
OTINA; HEMIASCOMYCETES
                                                                                                                                                                                                            CHAPMAN I
ECH T.R.;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
PTASE 1.
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Best Local Similarity 26.4%;
Matches 129; Conservative
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O13338 PRELIMINARY; PRT; 989 AA.
O13338;
O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLEEL. 05, LAST SEQUENCE UPDATE)
O1-JUN-1998 (TREMBLEEL. 06, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE 1.
                                                                                                                                                                                                                                                                                                                        NAKAMURA T.M., MORIN G.B., CHAPMAN K.B.,
LINGNER J., HARLEY C.B., CECH T.R.;
SCIENCE 277:955-959(1997)
EMBL; AF015783; G2340169; -.
PFAM; PF00078; TVT.
RNA-DIRECTED DNA POLYMERASE.
SEQUENCE 989 AA; 116456 MW; FDE74202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 97400623.
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                                                                                                                                                                                                                                    Local
EWLVLGKRSNAKMCLSDFEKR-KQ-IFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTV 457
                                                                                          PWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDC 539
                                                                                                                                                PNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEI 399
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AWL---RRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLF 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFV
                                                                                                                                                                                                      Ch 7.9%; Score 681; DB 3; IA 1 Similarity 26.3%; Pred. NO. 3.12e-111; 129; Conservative 136; Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    963
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Pred. No. 1.37e-110;
                                                                                                                                                                                                                                                                                                                              FDE74202 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEINRICH
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                                                                                                                                                                                                                                                            Length 989,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.L.,
                                                                                                                                                                                                            Indels
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Best Local Similarity 23.0%;
Matches 142; Conservative
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O00939;

O1-JUL-1997 (TREMBLREL. 04, C

O1-JUL-1997 (TREMBLREL. 04, L

O1-JAN-1998 (TREMBLREL. 05, L

TELOMERASE SUBUNIT P123.
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EMBL; U95964; G2072336; -.
SEQUENCE 1031 AA; 12256
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HYPOTRICHS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A. EDLINE; 97274210.
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                                                      QVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVIDSKN
                                                                                                                                                                                                                                                                                                                                                                                    ETSAKHFYYFDHE-NIYVLWKLLRWIFEDLVVSLIRCFFYYTEQQKSYSKTYYYRKNIWD
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                                                                                                                                                             KIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCK-WK
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; Pred. No. 1.97e-60;
168; Mismatches 261;
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LAST SEQUENCE UPDATE)
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Best Local
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Q06163;
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O35432; PRELIMINARY; PRT; 67 AA.
O1-JAN-1998 (TREMBLREL 05, CREATED)
O1-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
TELOMERASE CATALYTIC SUBUNIT (FRAGMENT).
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA
                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
CHROMOSOME XII COSMID 8543.
L8543.12.
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ
EMBL; AF029235; G2605903;
SEQUENCE FROM N.A. STRAIN-S288C (AB972);
MEDLINE; 97313267.
JOHNSTON M., HILLIER L.,
                                                                                                                          SACCHAROMYCES CEREVISIAE (BAKER' EUKARYOTA; FUNGI; ASCOMYCOTINA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 RLRFIPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPVIN-ICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPE 769
                                                                                                                                                                                                                                                                                                                                                                                                                           RLRFIPK
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larity 76.1%;
Conservative
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  RILES
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Pred. No. 2.25e-57;
10; Mismatches 6
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Best Local
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ENTIAN K.D., FLOETH M., GOFFERAU A., HEBLING U., HEUMANN K.,
HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,
LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTI D.,
MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M.,
PORTETELLE D., PURNELLE B., RECHMANN S., RIEGER M., RINKE M., ROSE I
SCHARFE M., SCHERENS B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,
UNDERWOOD A.P., URRESTARAZU L.A., VANDENBOL M., VERHASSELT P.,
UTERENDEELS E., VOET M., VOLCKAERT G., VOSS H., WAMBUTT R., WEDLER
WEDLER H. WEDLER T. T., WEDLER T. MEDLER T. M
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STRAIN-S288C (AB972);
CHERRY J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA EMBL; U20618; G662136; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDLER H., ZIMMERMANN F.K., ZOLLNER A., HANI J., NATURE 387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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        939 TAFVOM
                                                                               718
                                                                                                                                                               879 IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGG
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                                                                               IQFCAM
                                                                                                                                                                                                                                                                                                                          EASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDM-E-NKLF-AG
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l Similarity 24.3%;
l18; Conservative
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; Pred. No. 1.71e-35;
122; Mismatches 202
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RESULT 9 ID Q69118 AC Q69118;

PRELIMINARY;

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296 AA.

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321 VGRQHHAGPPSTSRPPRPWDTPCPPV

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RESULT 10

ID 36027;
AC 036027;
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AC 01-JUN-1998
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AUSKOTT ALDR.
SPACE
OS SCHIZOSACCHA
AC EUKARYOTA; FI
RN [1]
RP SEQUENCE FRO;
RL SUBMITTED (SI
RN [2]
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CC -!- SIMILARII
DR EMBL; AF0385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG 1
WSP1 OR SPAC4F10.15C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 87284169.
PRITZNER A.J., TSAI E.C., STROMINGER J.L.,
J. VIROL. 61:2902-2909(1987).
EMBL; M17294; G807646; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZANKEL T.C., OW D.W.;
SUBMITTED (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-JS21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMMAHERPESVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN HERPESVIRUS TYPE 4.
VIRIDAE; DS-DNA ENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          305
  417
                                                                                              359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :- SIMILARITY: TO YEAST LAS17.
EMBL; AF038575; G2708709; -
                                                 262
                                                                                                                                             202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                           ;; Z98980; E339884; -.
IN 311 317
IN 311 343
IN 361 366
ANT 248 248
ANT 248 248
                                            AANKKRPPPPPP-PSRR---NRG-KPPIGNGSSNSSLPPPPPPPPRSNAAG-SIPLPPQGR 358
                                                                                                                                           AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASRSLPLPKRPRRGAAPEPER-TPVGQGSWAHPGRTRGPSD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPLYQLGAATQARPPPHASG-PRR-R-LGCERAWNHSVREAGVPLGLPAPGA-RRRGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPPPTRSGAAAQ-RTHRRPPGCPRSARNPGCPRTWRR--R-SGAQRGHPPPGAGQRPSGP 146
VPTPP-SLPPSAPPSLPPSAPPSLPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPAD 187
                                                                                                                                                                                                                                                                                                                                  311
337
361
348
248
574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNGI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AA; 31393 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TREMBLREL. 06, CREATED)
(TREMBLEL. 06, LAST SEQUENCE UPDATE)
(TREMBLEL. 06, LAST ANNOTATION UPDATE)
RICH SYNDROME PROTEIN HOMOLOG 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7%;
larity 38.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                             1.7%;
28.8%;
                                                                                                                                                                                                                                                                                                                                       59605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                                         POLY-PRO.
POLY-PRO.
POLY-PRO.
L -> V (IN STRAIN JS21).
W; 9E84D37C CRC32;
                                                                                                                                                                                                                                    Score 143; DB 3; Le Pred. No. 2.85e-05; 41; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 147; DB 14;
Pred. No. 7.18e-06;
20; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D17CEF6F
441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECK S.
                                                                                                                                                                                                                                                                                      Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WOOD
                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249
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RESULT 12
ID Q46612;
AC Q46612;
DT Q46612;
DT 01-NOV-1996 (TREMBLREL. 01, CRE
DT 01-NOV-1996 (TREMBLREL. 06, LAS
DT 01-JUN-1998 (TREMBLREL. 06, LAS
DT 01-JUN-1998 (TREMBLREL. 06, LAS
DE IS 1222 GENE ORF-A AND ORF-B.
OS ENTEROBACTER AGGLOMERANS.
OC PROKARYOTA; GRACILICUTES; SCOTO
OC ENTEROBACTERIACEAE.

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KLEEBERGER, 1983;
RX MEDLINE; 9525664.
RA STEIBL H.D., LEWECKE F.M.;
RL GENE 156:37-42(1995).
RN [2]
RP SEQUENCE FROM N.A.
STEIBL H.D., SIDDAVATTAM D.;
RL SUBMITTED (AUG-1996) TO EMBL/GE
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96422758.
RA STEIBL H.D., SIDDAVATTAM D., KL
RL PLASMID 34:223-228(1995).
RN [4]
RP SEQUENCE FROM N.A.
RA STEIBL H.D.;
RN [4]
RP SEQUENCE FROM N.A.
RA STEIBL H.D.;
RN [4]
RP SEQUENCE FROM N.A.
RA STEIBL H.D.;
RN [4]
RP SEQUENCE FROM N.A.
RA STEIBL H.D.;
RR EMBL; X81893; E258949; -
SQ SEQUENCE 276 AA; 31718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN INC. TO SEE THE PROPERTY OF SECOND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δõ
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Best Local Similarity
Matches 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDILINE; 96108975.
AZEN E.A., AMBERGER E., 1
AM. J. HUM. GENET. 58:14:
AM. J. HUM. GENET. 58:14:
EMBL; S80916; G1911492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000600
000600;
01-JUL-1997
01-JUL-1997
01-JUL-1997
PAROTID 'O'
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPAGKPQGPPPPPQGGRPPRP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 (TREMBLREL. 04, CREA
7 (TREMBLREL. 04, LAST
7 (TREMBLREL. 04, LAST
, PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%;
larity 28.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S8:143-153(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23656 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01, CREATED)
01, LAST SEQUENCE UPDATE)
06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                     EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 142;
Pred. No. 4
41; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                             BAYREUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
                                                                                                                                                                                                                                      KLINGMUELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B5920075 CRC32;
              0B54A420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No. 4.02e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRAKOBPHOL
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              CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FACULTATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽
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                                                                                                                                                                                                                                                                                                                                                     DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Α.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
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01-JUN-1998 (TREMBLREL. 06, CKEALE 01-JUN-1998 (TREMBLREL. 06, LAST 7 01-JUN-1998 (TREMBLREL. 07, LAST 7 POLYKETIDE SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.6%;
Best Local Similarity 30.9%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.6%;
Best Local Similarity 33.7%;
Matches 30; Conservative
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01-NOV-1996
01-JUN-1998
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Q99076;
                                         SALAH-BEY K., DOUMITH M., MICHEL J.M., HAY
LEADLAY P.F., RAYNAL M.C.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ
EMBL; Y14332; E1228185; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HB9.
HOMO SAPIENS (HUMAN).
HOMO SAPIENS (HUMAN).
CHORDATA;
                                                                                                                                   SEQUENCE FROM N.A. STRAIN-NRRL2338;
                                                                                                                                                                                                  SACCHAROPOLYSPORA ERYTHRAEA (STREPTOMYCES PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X56537; E30256; ALT_SEQ.
PIR; S16681; S16681.
  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEGUCHI Y., KEHRL J.H.;
NUCLEIC ACIDS RES. 19:3742-3742(1991).
-!- SIMILARITY: STRONG WITH OTHER "ANTP-TYPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-TONSIL;
MEDLINE; 91305125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPWSTASSDCSYGRTGIAPRGPAT-SPRPSRSPAAQDRSRPARSAPGPAASPGGPGAWTH 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARPREQA 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRV-QLRELSEAEVRQHREARPALLTSRL 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGRTRGPS 288
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112
316 AA;
  373 AA;
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(TREMBLREL.
(TREMBLREL.
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121 H
34713 MW;
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  40872 MW;
                                                                                                                                                                                                                                                                                     06, CREATED)
06, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 136; DB 4;
Pred. No. 3.03e-04;
20; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 141; DB 2;
Pred. No. 5.65e-05;
23; Mismatches 3(
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H-T-H MOTIF.
; 1531E766 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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  781BEC6D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                               373 AA.
                                                                                                            HAYDOCK S., CORTES
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                                                                DATA BANKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Job time :

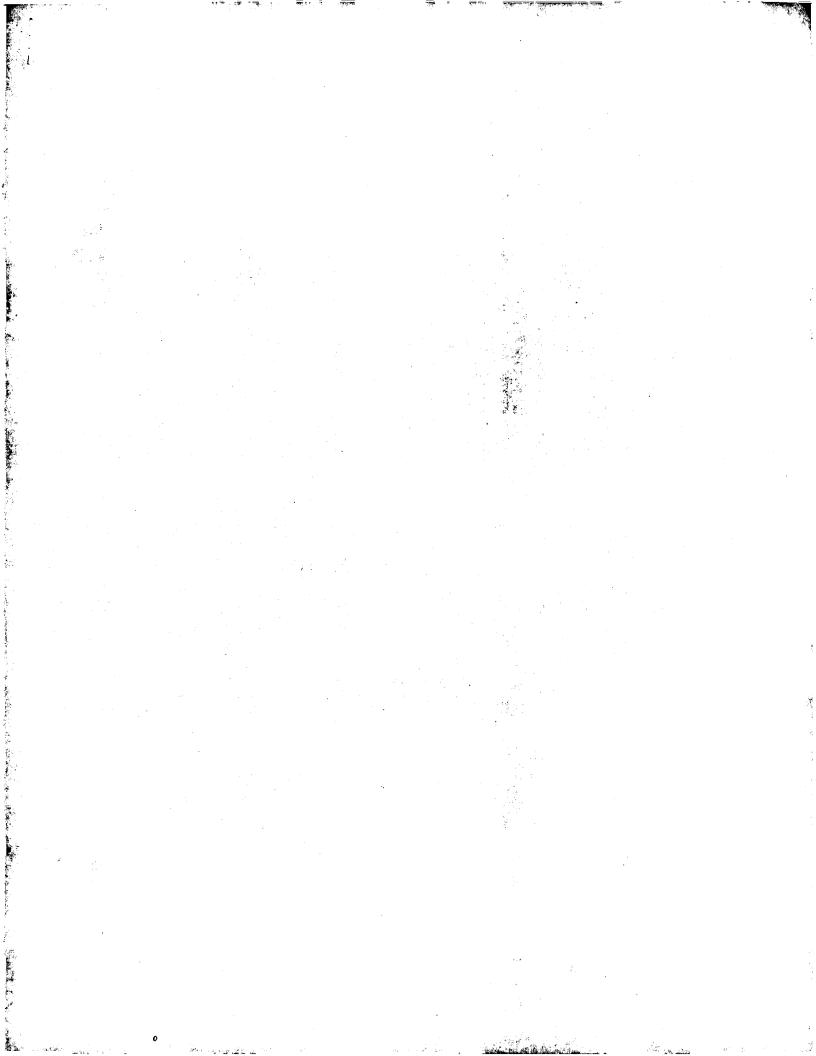
190 secs

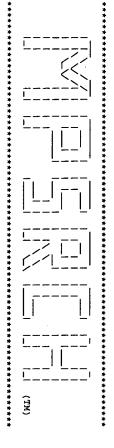
Search completed: Fri Dec

18

18:30:12 1998

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RESULT 15
ID 041935;
AC 041935;
AC 041935;
DT 01-JAN-1998 (TREMBLREL 05, CRE DT 01-JAN-1998 (TREMBLREL 05, LAS DT 01-JAN-1998 (TREMBLREL 05, LAS DT 01-JAN-1998 (TREMBLREL 05, LAS DE HYPOTHETICAL 60.2 KD PROTEIN.
GN MURINE HERPESVIRUS 68.
OC VIRUSES; DSDNA VIRUSES, NO RNA RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WUMS;
RA VIRGIN H.W. IV, LATREILLE P., W RA DAL CANTO A.J., SPECK S.H.;
RL J. VIROL. 71:5894-5904(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WUMS;
RA DAL CANTO A.J., SPECK S.H.;
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATREILLE P., WAMSLEY P., WATERSTON R.H.;
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U97553; G2317934; -.
HYPOTHETICAL PROTEIN.
     310
                                                          457
                                                                                                                 251
                                                                                                                                                                   401
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                                                                                                                                                                                                                                                                                  342
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Local Similarity 32.3%;
                                                                                                                                                                                                                                                                                                                                       1.6%;
Local Similarity 27.6%;
les 45; Conservative
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                                                                                                                                                  ARIPDLPGPLPSWGPDPRPPPELGP-GSPT-SPAPSRAGARIPRPSRPPPELGP--G
                                                                                                                                                                                                                           PPLYQLGAATQARPPPHASGPRRR-L-GCERAWNHSVREA-GVP-LGLPAPGARRRGGSA 250
                                                                                                                                                                                                                                                                               PPP-ELGPGSPTSPAPSRAGARIPDLPGPLPSWGPDPRPPPPELGPGSPTSPAPSRAG
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                                                       SPRFPRPSRPP--PELGPGSPDLPGPLPSWG-PDPPTFPAPSR
     ALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKH
                                                                                                                 SRSLPLPKR-PRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEG
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                       Score 135; DB 14;
Pred. No. 4.23e-04;
37; Mismatches 68
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Pred. No. 7.93e-05;
27; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WAMSLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         B35C72E5 CRC32;
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U Distribution rights by Oxford Molecular Ltd Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman.algorithm

Run on: Fri Dec 18 18:30:31 1998; MasPar time 9.93 Seconds 823.071 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

Sequence: >US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

Mean 37.265;

Variance 182.038; scale 0.205

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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APPLICATION NUMBER: US 660,162 FILING DATE: 22-FEB-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 621,988 FILING DATE: 04-DEC-1990	APPLICATION NUMBER: US 827,052 FILING DATE: 28-JAN-1992 PRIOR APPLICATION DATA:		A PON M: IS	Sequence 27, Application US/08147023 Patent No. 5468845 GENERAL INFORMATION: APPLICANT: OPPERMANN, HERMANN APPLICANT: OZKAYNAK, ENGIN APPLICANT: KUBERASAMPATH, THANGAVEL APPLICANT: RUGGER, DAVID C. APPLICANT: PANG, ROY H.L. TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: 53 STATE STREET CITY: BOSTON	US-08-147-023-27 STANDARD; PRT; 399 AA. xxxxxx sequence 27, Application US/08147023

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RESULT
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                                                                                                                                    US-08-447-570-27
                                                    Sequence 27, Application US/08447570
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
Patent No. 5714589
GENERAL INFORMATION:
                 Sequence 27, Application Patent No. 5714589
                                                                                                                                                                                                                                            194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                       254 LP 255
                                                                                                                                                                                                                                                                                      1.48;
Local Similarity 38.78;
les 24; Conservation
                                                                                                                                                                                                                 68 QP 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 232,630
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PRIOR APPLICATION NUMBER: US 579,865
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PRIOR APPLICATION NUMBER: US 600,024
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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REFERENCE/DOCKET NUMBER: CR
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                                                                                                                                    STANDARD;
                            US/08447570
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Pred. No. 2.06e+00; 
12; Mismatches 22; Indels
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    APPLICANT:
APPLICANT:
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FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 23
FILING DATE: 15-AUG-1988
                                                                                                                                                                                                                FILING DATE: 22-FEB-PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5:
FILING DATE: 07-SEP-1990
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FILING DATE: 21-NOV-
PRIOR APPLICATION DATA:
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                         FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
                                                                                                                                                                           PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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    TELECOMMUNICATION INFORMATION:
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 569,920 FILING DATE: 20-AUG-1990
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                 REFERENCE/DOCKET NUMBER:
                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                          APPLICATION NUMBER:
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53 STATE STREET
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OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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IBM PC compatible
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04-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application PC/TUS9201968 GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/019
FILING DATE: 19920311
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: US 752,764
APPLICATION NUMBER: US 752,764
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                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSEE: TESTA HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE 53 STATE STREET
                                                                                                REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
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APPLICANT: RUEGER, DAVID C
TITLE OF INVENTION: PROTEIN-INDUCED MORPHOGENESIS
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JENCE 399 AA; 44764 MW; 790568 CN;
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LENGTH: 399 amino acid
                                                                                                                                                                                                     FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
TERRET TO THE PARTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP:
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                                                                                                                                                                          NAME: PITCHER ESQ, EDMUND R REGISTRATION NUMBER: 27,829
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Pred. No. 2.06e+00;
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Matches
Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                          ZIP: v1/32
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: DOS/MS-DOS
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APPLICANT:
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TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
                                                                                                                                                                  APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESq., EDMUND R.
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: 27,829
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                                                                                                                                               REFERENCE/DOCKET NUMBER: CR
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Similarity 38.7%;
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OZKAYNAK, ENGIN
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RUEGER, DAVID C.
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                                                                                                                                      (508) 435-9001
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, 435-6951
NO: 23:
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Pred. No. 2.06e+00;
Pred. no. 2.2;
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Score 118; DB 1;
Pred. No. 2.06e+00;
12; Mismatches 22
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Best Local (
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/643,763A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REGISTRATION NUMBER: 36,508
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                                                                                                   Local Similarity
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
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REFERENCE/DOCKET NUMBER: CRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEPAX
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MORPHOGENIC-I
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                                             GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
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38.7%;
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23:
                                                                                      Score 118; DB 1; Length 399; Pred. No. 2.06e+00; 12; Mismatches 22; Indels
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Best Local :
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                                 Sequence 23, Application US/08643563A
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Sequence 23, Application US/08643563A Patent No. 5707810
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NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 19920616
CLASSIFICATION: 435
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Similarity 38.7%;
24; Conservative
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OZAKAYNAK, ENGIN
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KUBERASAMPATH, THANGAVEL
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Pred. No. 2.06e+00;
12; Mismatches 22;
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GENERAL INFORMATION:

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Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                                     Sequence 10, Application US/08479666
                                                                                                                                                                                         US-08-479-666-10
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                                                                                                Sequence 10, Application US/08479666
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                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
JENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY ESQ., MICHAEL J.
REGISTRATION NUMBER: 38,349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
                               APPLICANT:
                                                     APPLICANT:
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TITLE OF INVENTION:
                      APPLICANT:
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CITY: HOPKINTON
STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 06-MAY-1996 CLASSIFICATION: 435
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                                                                                       56523
                   OPPERMANN, HERMAN
OZKAYNAK, ENGIN
KUBERASAMPATH, TH
RUEGER, DAVID C.
PANG, ROY H.L.
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OZKAYNAK, ENGIN
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          COHEN, CHARLES M.
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                                                                                                                                                                                         STANDARD;
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OP3-INDUCED MORPHOGENESIS
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                                                                 HERMANN
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Pred. No. 2.06e+00;
12; Mismatches 22; Indels
                                            THANGAVEL
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Best Local Similarity 38.7%;
Matches 24; Conservative
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                                                                                                                                                                                                                               Sequence 23, Application US/08155343A
                                                                                                                                                                                                                                                                                                    US-08-155-343A-23
                                                                                                                                                                                                                                                                                                                                                                                             194 GPPLYQLGAATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
                                                                                                                                                                                Sequence 23, Application US/08155343A Patent No. 5656593 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  254 LP 255
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TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                                                                                                                                                                      68 QP 69
                                                                                                                                                                                                                                                                                                                                                                                                                  12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,666
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                 NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                       APPLICANT: OPPERMANN, HER APPLICANT: COHEN, CHARLES APPLICANT: PANG, ROY H.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FENTON ESG., GILLIAN M. REGISTRATION NUMBER: 36,508 REFERENCE/DOCKET NUMBER: CRPTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: FENTON ESG., GILLI
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COMPUTER READABLE FORM:
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                                                                                                   TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE TITLE OF INVENTION: REGENERATION.
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            COUNTRY: U
ZIP: 01748
                                  STATE:
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OPPERMANN, HERMAN
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                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                      CHARLES M.
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pred. No. 2.06e+00;
12; Mismatches 22
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Floppy disk

MEDIUM TYPE: COMPUTER: II

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Matches 2
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Local Similarity 38.7%;
nes 24; Conservative
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APPLICATION NUMBER: PCT/US93/
FILING DATE: 1930729
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 23:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      TITLE OF INVENTION: MO
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FENTON ESQ., GILLIAN M. REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                 STREET: 35 SOUTH CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08 FILING DATE: 15-NOV-1993
                                                                                                                                                                                             COUNTRY: USA
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35 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                  MORPHOGEN-INDUCED NERVE REGENERATION AND REPAIR
33
                                                                                                PCT/US93/07231
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Pred. No. 2.05e+00;
12; Mismatches 22;
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Best Local :
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                                                                        SEQUENCE
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NAME: A-REGISTRATION NUMBER: STK-REFERENCE/DOCKET NUMBER: STK-TELECOMMUNICATION INFORMATION: 617/248-7000
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Local Similarity 38.7%;
hes 24; Conservative
                                        Match 1.48;
Local Similarity 38.78;
                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 399 amino acid
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INFORMATION FOR SEQ ID NO:
                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 399 AA; 44764 MW; 790568 CN;
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05446
FILING DATE: 19930608
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ, EDMU
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 399 amino acid
                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                        TYPE:
                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                      AMINO ACID
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                                Conservative
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                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           PROSTHETIC DEVICES HAVING ENHANCED OSTEOGENIC PROPERTIES
                                                                                                                                                                                         EDMUND R
                                12; Mismatches 22; Indels
                                        Score 118; DB 2;
Pred. No. 2.06e+00;
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Pred. No. 2.06e+00;
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      Query Match 1.4%;
Best Local Similarity 38.7%;
Matches 24; Conservative
                                         SEQUENCE
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                                                                                                          FILING DATE: 31-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
                                                                                         TELEPHONE: (508)435-9001
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                 APPLICATION NUMBER: US 07/923,780
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION TOTAL
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/667,274
FILING DATE: 11-MAR-1991
PRIOR APPLICATION NUMBER: US 07/752,764
FILING DATE: 30-AUG-1991
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10520
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acid
                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/753,059 FILING DATE: 30-AUG-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: OP NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             APPLICATION NUMBER: US 07/752,857 FILING DATE: 30-AUG-1991 PRIOR APPLICATION DATA:
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                                        MOLECULE TYPE: protein
ENCE 399 AA; 44764 MW; 790568 CN;
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                                                         TOPOLOGY:
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             Score 118; DB 2;
Pred. No. 2.06e+00;
        12;
        Mismatches
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                                                                                                                                68 QP 69
                                                                                                                                                                                                                                                 Match 1.48;
Local Similarity 38.78;
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TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 23:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARD.
                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
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Pred. No. 2.06e+00;
12; Mismatches 22;
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Sequence 23, Application US/08462623

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Best Local Similarity 38.7%;
Matches 24; Conservative
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                                 Sequence 8, Application PC/TUS9307189
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GENERAL IN
Sequence 8, Application PC/TUS9307189 GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/445,8
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
                                                                                                                                                                    68 QP 69
                                                                                                                                                                                                             12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                                                                                                                                                                       TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
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APPLICANT:
APPLICANT:
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MOLECULE TYPE: protein
UENCE 399 AA; 44764 MW; 790568 CN;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                  STANDARD;
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Pred. No. 2.06e+00;
Pred. No. 2.06e+20;
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Search completed: Fri Dec 18 18:31:03 1998 Job time : 32 secs.

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Best Local Similarity 38.78;
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                                              194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS 253
  254 LP
                       68 QP 69
                                                            12 GLALCALGGGHGPRPP-HTC-PQRRLG-ARERRDMQREILAVLGLPGR-PRPRAQPAAAR 67
                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 399 amino acids
                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
FILING DATE: 19930729
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
                                                                                                                                                        TYPE: ami
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Pred. No. 2.06e+00;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Dec 18 18:31:23 1998; MasPar time 55.03 Seconds 793.597 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-08-951-733-20 (1-1154) from US08951733.pep 8624 1 HASGQRCVLLRTWEALAPAT......TALEAAANPALPSDFKTILD 1154

Scoring table: PAM 150 Gap 11

Searched: 321025 seqs, 37841481 residues

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Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-pending 1:P9 2:U60 3:U7 4:U80 5:U81 6:U82 7:U83 8:U84 9:U85 10:U86 11:U87 12:U88 13:U89 14:U90 15:U91 16:NEWP 17:NEWU6 18:NEWU8 19:NEWU9

Statistics: Mean 40.459; Variance 196.267; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8624 8607 8607 8607 8607 8607 8607 8607 8590 8465 8465 8465 8465 8465	Score
100 988888899999999999999999999999999999	% Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino act
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TYPE: amino acid
STRANDEDNESS: unkno
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKA 780
                                                                                                                                                                                        WLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTTFQKNRLFFYRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCAL
                                                            FKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAV
                                                                                                                                                       VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVR
                                                                                                                                                                                                                                                                                    WQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCA
                                                                                                                                                                                                                                                                                                                 NHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSP
                                                                                                                                                                                                                                                                                                                             NHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSP
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                                                                                                                                                VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVR
                                                                                                                                                                                                                                 WLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRK
                                                                                                                                                                                                                                                                         WQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCA
HAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTR
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Similarity 100.0%;
154; Conservative
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Pred. No. 0.00e+00;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Ca
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
       APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR 1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANPALPSDFKTILD
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                                                                                                                                                         APPLICATION NUMBER: US 08/724,643 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19-NOV
                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                   California
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 US 08/911,312
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Matches 115
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 613:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, RANDOLPh Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                                                                                                                                                                 97
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
APPLICATION UNBER: 14-AUG-1S
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein LOCATION: 1.1189
OTHER INFORMATION: /n:
OTHER INFORMATION: me
OTHER INFORMATION: hT
ENCE 1189 AA; 133179 M
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                                                                                                                                                                                                    GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA 336
                                                                                                                                                                                                                                                    VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
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                                                                                                QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                                                                                                                 EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE
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                                                             HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                     QLRPSFLLSSLRPSLTGARRLYETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                                                                                                      EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE
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Conservative
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Pred. No. 0.00e+00;
0; Mismatches 1
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                                               Sequence 34, Application US/08911312
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Gregg B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reve
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                    NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Townsend and Townsend
Townsendero Center, J
                                                                                                                                                                                                                                                                        NPALPSDFKTILD
                                                                                                                                                                                                                                                                                                                                                   LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT
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                                                                                                                                                                                                                                         NPALPSDFKTILD
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                                                                                                                                                                                                                                                                                                                                           LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT
                                                                                                                                                     34,
                San Francisco
                                                                                                                                                     Application US/08911312
        California
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                                                                                                                                                                                                        STANDARD;
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                                                           Reverse Transcriptase
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Best Local Similarity 99.9%;
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FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
14-AUG-1997
AFTORNEY/AGENT INFORMATION:
ANAME: 11-AUG-1997
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
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                               GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA
                                                                        EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHELYSSGDKE
                                                                                                                    GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
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                                                                                                                                                                                                                                                 1152;
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OPERATING SYSTEM:
SOFTWARE: Patent
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 015389-002500US
                                                                                                                                                                                                                                                                                         LE TYPE: protein
1189 AA; 133179 MW; 7256545 CN;
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SYSTEM: PC-DOS/MS-DOS
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18-APR-1997
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NO: 34:
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                                                                                                                                          Sequence 325, Application US/08912951
  Sequence 325, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linguer, Joachim
APPLICANT: Nakamura, Toru
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157 GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF 216
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MOLECULE TYPE: protein
UENCE 1189 AA; 133179 MW; 7256545 CN;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 01-OCT-
CLASSIFICATION: 435
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ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor
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APPLICANT: Anddrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
TITLE OF INVENTION: THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                    ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 96
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STATE: California
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Harley, Calvin
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	15		Qy
	ALPSDFKTIL	1177	Дb
1141	GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA	1082	γo
1176	AAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA	1117	Дb
1081	LGAK	1022	Qy
1116	IYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK	1057	рb
1021	SLFLDLQVNSLQTVCT	962	Qy
1056	EVQSDYSSYARTSIRASLTENRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT	997	Db
961	WCGLLLDTRT	02	Qy
996	FLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT	937	Db
901	GKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH	842	Qy
936	RGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH	877	Db
841	GLFDVFLRFMCHHAVR	782	Qy
876	SHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR	817	당
781	ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF	722	Qy
816	DPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF	757	В
721	VRA	662	Qy
756	ARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA	697	Db
661	IVMMYV	602	Qy
696	SIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV	637	DЬ
601	YRKS	542	Qy
636	RRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS	77	망
541	RACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW	N	Qy
576	GFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW	517	Db
481	MdS	22	Qy
516	QCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW	457	Db
421	SFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN	362	Qγ
456	LRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN	397	DЪ
361	EATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE	302	Qγ
396	AETKHFLYSSGDKE	337	망
301	ARPA	242	Qy
336	ARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA	277	В
241	VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP	182	Qy
276	VAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP	217	B
181	GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF	122	Qy

RESULT ID US

US-08-974-549-612

STANDARD;

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Sequence 612, Application US/08974549
GENERAL INFORMATION:
INFORMATION FOR SEQUENCE CHARA
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
TITLE OF INVENTION: Human Telomerase Catalytic &
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                    APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
                                                                                                                               APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
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FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 09-MAY-1997
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                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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PRIOR APPLICATION DATA:
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                                                        REFERENCE/DOCKET NUMBER: 015389-002610US
                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/912,951 FILING DATE: 14-AUG-1997
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FILING DATE: 19-NOV-1997
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STATE: California
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N FOR SEQ ID NO:
CHARACTERISTICS:
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Chapman, Karen B.
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14-AUG-1997
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25-APR-1997
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NAME/KEY: Protein
LOCATION: 1.1200
OTHER INFORMATION: /n
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 KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR
                                               VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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2 MW: 7387257 CN;
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                                      APPLICATION NUMBER: US 08/
FILING DATE: 09-WAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-WAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT:
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT
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                           FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 14-AUG-1997
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                         STREET: Two Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   94111
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Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                             United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas R.
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                                                                                                             US 08/854,050
                                                                                                                                                                    us/08/912,95
 US 08/846,017
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                                                        08/851,843
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Best Local Similarity 99.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 0153(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAC: (415) 576-0300
INFORMATION FOR SEQ ID NO: 324:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
                                                                                                                                                                                                                                                                            648
                                                                                                               482
                                                                                                                                                                                                                                                                                                                                     242
                                                                                                                                                                                                                                                                                                                                                                                                        228 VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF
                                                                                                                                                                                                                         362 QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
               VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLISRLREIPKPDGLRPIVMMDYV
                                                                     LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                            QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                                                                               HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                                                                                                                                                                      QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
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                                                                                                             QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                                                                  HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
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  VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
                                                        LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS
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TOPOLOGY: 11
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TYPE: amino acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LE TYPE: protein
1200 AA; 134322 MW; 7387257 CN;
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Pred. No. 0.00e+00;
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                                                                                                                                                                                           APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/911,312
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPALPSDFKTILD 1200
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                                                                                                    COUNTRY: USA
ZIP: 94111-3834
                                                                                                                               CITY: San Francisco
STATE: California
                                                                                                                                                       STREET:
                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                     33, Application US/08911312
                                                                                                                                                       E: Townsend and
Two Embarcadero
                                                                                                                                                                                                                                                                                                     Cech, Thomas R.
 14-AUG-1997
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                                                                                                                                                       Townsend and Crew LLP
Center, Eighth Floor
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
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FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 06-MAY-1997
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
FILING DATE: 18-APR-1997
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MENCE 1200 AA; 134322 MW; 7387257 CN;
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FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P
                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                            QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 167
                                                                                                                                                                                                                                                                                                                                              ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 107
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 HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
            HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTIDPRRLVQLLRQHSSPW
                                              QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
                                                          QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN
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FILING DATE: 09-MAN
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TOPOLOGY: linear
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14-AUG-1997
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09-MAY-1997
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APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYYGFYRACLRRLYPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSYRDCAW
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Best Local S
Matches 115
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LOCATION: 1.1285
LOCATION: /n
OTHER INFORMATION: /n
OTHER INFORMATION: en
OTHER INFORMATION: th
SEQUENCE 1285 AA; 143529 M
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FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION NUMBER: US 08/854,050
FILING DATE: US 08/854,050
FILING DATE: 09-MAY-1997
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino aci
                                                                                                                                                                                                                                                                                                                                                                      NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36.429
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO P
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/US97/17618 FILING DATE: 01-OCT-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     FEATURE:
                                        ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 192
                         ASGORCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 61
                                                                                al Similarity
1152; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
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California
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                                                                                               99.88;
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                                                                                                                                          /note= "fusion protein composed of enterokinase cleavable, His tagged thioredoxin modety and full length 9 MW; 8449280 CN;
                                                                                                                                                                                                                                                                                                               acids
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                                                                                Score 8607; DB 18;
Pred. No. 0.00e+00;
0; Mismatches 1;
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                                                                                                             Length 1285
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Sequence 600, Application US/08974549
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Morin, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.

Sequence 600, Application US/08974549

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GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1272
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                               GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA
                                                                                              NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK
                                                                                                                                                               LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAQCPYGYLLKTHCPLRAAVTPAAGYCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
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                                                                                                                                                                                                                                    APPLICATION UNMBER: US 08/844,419
ETILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/846,017
ETILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/851,843
ETILING DATE: 06-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/854,050
ETILING DATE: 09-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/854,050
ETILING DATE: 09-MAX-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/912,951
ETILING DATE: 14-AUG-1997
                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Re
NUMBER OF SEQUENCES: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
                                                                                      NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,40
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION UMBER: US//8/911,312 FILING DATE: 14-AUG-1997
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CORRESPONDENCE ADDRESS:
Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                           APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY,AGENT INFORMATION:
NAME: Einhorn, Gregory P.
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ZIP: 941
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 STRANDEDNESS:
                               LENGTH:
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14-AUG-1997
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LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT 1152
                                                                                                           KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 972
                                                                                                                                                                                                          VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA 852
                                                                                                                                                                                                                                                       VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV 792
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                    IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH 1032
                                                                                                                                                                QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF 912
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Similarity 99.9%;
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1285 AA; 143529 1
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APPLICANT: NAKAMURA, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 314, Application GENERAL INFORMATION:
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,05
EILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/851,84
EILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,01
EILING DATE: 25-APR-1997
CIASSIFICATION NUMBER: US 08/846,01
                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 14-AUG
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CITY: San Francisco
STATE: California
APPLICATION NUMBER: US 0 FILING DATE: 01-OCT-1996 CLASSIFICATION: 435
                                                      APPLICATION NUMBER: US 0 FILING DATE: 18-APR-1997
                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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14-AUG-1997
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                     US 08/724,643
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Center, 8th Floor
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INFORMATION FOR SEQ ID NO: 314:
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REGISTATION NUMBER: 36,429
REFERENCION NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                         VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                      QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF
                                                                                                                                           VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLISRLREIPKPDGLRPIVMDYV
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KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR
                       QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF
                                                                          VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
                                                                                                                               VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
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TOPOLOGY: 11
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larity 99.9%;
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Pred. No. 0.00e+00;
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CC GENERAL INFORMAN
CC APPLICANT: Li
CC APPLICANT: M
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APPLICATION UMBER: US/08/S
FILING DATE: 14-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 55, Application US/08911312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 170
                                                     FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
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                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
     APPLICATION NUMBER: US 08/846,017 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
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CITY: San Francisco
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Best Local Similarity 99.7%;
Matches 1150; Conservative
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REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14 AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1407 AA; 157668 MW;
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PRIOR APPLICATION DATA:
US
OTHER PRIOR NUMBER: US
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APPLICATION NUMBER: US 0
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
                                                                                                                                                               LRRSPGVGCVPAAEHRLREEILAKFLHWIMSVYVVELLRSFFYVTETTFQKNRLFFYRPS
                                                                    QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW
                                                                                                                              HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
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VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV
                                                                                                                   HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW
                                                                                                                                                                                                              EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE
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TYPE: a
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                         Sequence 628, Application US/08974549 GENERAL INFORMATION:
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       STREET: Two Embarcadero Center, E1(
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                     APPLICANT: Cech, Thomas R.
APPLICANT: Nakamura, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Harley, Calvin H.
APPLICANT: Addrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      12
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEVQSDYSSYARTSIRASVTENRGEKAGRNMRRKLEGVLRLKCHSLELDLQVNSLQTVCT 1274
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                                                                                                                  ADDRESSEE: Townsend and
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION UNUBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION UNUBER: US 08/915,503
APPLICATION UNUBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
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ETLING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: APPLE, Randolph Ted
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 0153
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                           2
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APPLICATION NUMBER: US 08,
ETILING DATE: 01-CCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
ETILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                  NAME/KEY: Protein
LOCATION: 1.1407
OTHER INFORMATION: /n
OTHER INFORMATION: en
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OTHER INFORMATION: hT
OTHER INFORMATION: hT
                                                                                                                         ASTQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 314
              GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF 434
                                                                     QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF 374
                                                                                                           ASGQRCVLLRTWEALAPATPAMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLV 61
 GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF
                                                     QRGDPAAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAF
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FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino
STRANDEDNESS:
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enhanced green fluorescent prote
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                                                                                                                                                               Score 8590; DB 18;
Pred. No. 0.00e+00;
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                                                                             AKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT
                                                                                                                                                                                                IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH
                                                                                                                                                                                                                                     KSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR
                                                                                                                                                                                                                                                                           VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP
                                                 GAAGPLPSEAVQWLCHQAFLLKLITRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA 1394
                                                                                                                                                                                                                                                                                                                            VGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA
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  NPALPSDFKTILD
                                       GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA
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RESULT
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US-08-912-951-334

STANDARD;

PRT;

1407 AA

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          Query Match 99.6%;
Best Local Similarity 99.7%;
Matches 1150; Conservative
                                                                STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: |
SEQUENCE 1407 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: 25-APR-1997
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                  TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lingher, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC ANI
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                       amino acid
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                                                                                                                                     1407 amino acids
                                                                                                                                                            (415) 576-0300
TD NO: 334:
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                                                                                              linear
                                                                protein
157668 MW; 10134798 CN;
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           Score 8590; DB 13;
Pred. No. 0.00e+00;
1; Mismatches 2;
                                     Length 1407;
            Indels
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1394	GAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAA	1335	dd dd	
1081	NIYKILLLQAYREHACVLQLPEHQQVWKNPTEELRVISDTASLCYSILKAKNAGMSLGAK	1022	Qy	
1334	NIYKILLLQAYRFHACVLQLPFHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAK	1275	ДĎ	
1021	LEVQSDYSSYARTSIRASLTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT	962	Qy	
1274	LEVQSDYSSYARTSIRASVTFNRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCT	1215	dg dg	
961	LRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT	902	Qy	
1214	FLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRT	1155	dd	
901	IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH	842	Qy	
1154	IRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTH	1095	Db	
841	KSHYSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR	782	Qy	
1094	KSHV	1035	Db	
781	QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF	722	Qγ	
1034	QDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAF	975	ДĎ	
721	VGARTFRREKRAERLISRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA	662	Qy	
974	VGARTFRREKRAERLISRVKALFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLRVRA	915	Db	
661	VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV	602	Qy	
914	VWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYV	855	Db	
601	LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS	542	Qy	
854	LRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRPS	795	Дb	
541	QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW	482	Qy	
794	QVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAW	735	DЪ	
481	HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW	422	ν	
734	HAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPW	675	da	
421	QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN	362	Qγ	
674	QLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGN	615	Дb	
361	EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE	302	. Оу	
614	EEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKE	555	дb	
301	GARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA	242	Qy	
554	GARRRGGSASRSLPLPKRPRRGAAPEPERTPYGQGSWAHPGRTRGPSDRGFCVVSPARPA	495	ДЬ	
241	VLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP	182	Оу	ND
494	VLVAPSCAYOVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAP	435	ф	
181		122	Qy	
434	GFALLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALF	375	Db	
121	QKSIPAAF KALVAQCLV V YWDAKF PFAAFSE KQYSCLAKEVAKY LQKLLEKGAKNY LAF 	62	Q U	
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                             APPLICATION NUMBER: US 0 FILING DATE: 14-AUG-1997 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
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                                                                                    PRIOR APPLICATION DATA:
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                        APPLICATION NUMBER: FILING DATE: 01-00
                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 14-AUG-1997
                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
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Harley, Calvin B.
Andrews, William H.
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Chapman, Karen B.
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                        UMBER: WO PCT/US97/17618
01-OCT-1997
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                                                                          US 08/915,503
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mes 1132;
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LENGTH: 1132 amino aci
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                                                                                                                                                                                                                        RHNERRFIRNTKKFISLGKHAKLSLQELTWKMSVRDCAWIRRSPGVGCVPAAEHRLREEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                       PAAGVCAREKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGS
                                                                                                                                                                                                                                                                                                                                       VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
QETSPLRDAVVIEQSSSLNEASSGLEDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL
                        PODRLTEVIASIIKPONTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLOPYMROFVAHL
                                     PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL
                                                                       LSEAEVROHREARPALLISRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLISRVKA
                                                                                                                                     LSEAEVROHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
                                                                                                                                                                           LAKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRE
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                                                                                                                                                                                                                                                                                                                                                                           RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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Similarity 100.0%;
132; Conservative
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1132 AA; 126995 MW;
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ER: 015389-002610US
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                                                                             COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
ABBITICATION DATA:
ABBITICATION DATA:
ABBITICATION DATA:
ABBITICATION DATA:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Harley, Calvin
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC
TITLE OF INVENTION: THERAPEUTIC METHODS
                               APPLICATION NUMBER: US 0 FILING DATE: 06-MAY-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                    STREET: Two Embarcade
CITY: San Francisco
STATE: California
COUNTRY: United State
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
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                                                                                                                                                                                                                 MEDIUM TYPE:
COMPUTER: II
                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 California
United States
                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
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            25-APR-1997
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                       US 08/846,017
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Best Local (
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 mino acids
            661
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/724.
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: APPLe, Randolph T.
REGISTRATION NUMBER: 36,429
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                 LSEAEVRQHREARPALLISRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLISRVKA 660
                                                                               VETIFIGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT
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                                                                                                                                                                                                                                                                                                                                         GAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPPEAFTTSVR
                                                                                                                                                         RHNERRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI
                                                                                                                                                                                                                                                                             RQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYSSGDKEQLRPSFLLSSLRPSLTGARRL
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Similarity 100.0%;
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1132 AA; 126995 MW;
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ğ	721	-	780
Σ¥	743	PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL	802
ઠ	781	-	840
Ϋ́	803	QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILSTL	862
8	841	L	900
Ŋ	863	LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNL	922
용	901		960
Ϋ́	923	RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF	982
ઠ	961	0	1020
Δy	983	NRGFKAGRNMRRKLFGVLRLKCHSLFLDLQVNSLQTVCTNIXKILLLQAYRFHACVLQLP	1042
용	1021	-	1080
Ϋ́	1043	FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL:	1102
ઠ	1081	KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132	
Δy	1103	KLTRHRVTYVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1154	

Search completed: Fri Dec 18 18:34:40 1998 Job time : 197 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Dec 18 18:17:21 1998; MasPar time 8.35 Seconds

Run on: Fri Dec 18 18:17:21 1998; MasPar time 8.35 Seconds 804.709 Million cell updates/sec Tabular output not generated.

Title: >US-08-951-733-14
Description: (1-949) from US08951733.pep (1 of 2)
Perfect Score: 7113

Sequence: 1 HASGQRCVLLRTWEALAPAT.....PVEDEALGGTAFVQMPAHGL 949

Scoring table: PAM 150 Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 36.658; Variance 177.719; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222221188223333333333333333333333333333	Result
125 125 125 125 125 125 125 125 125 125	Score
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Length DB
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US-08-643- US-08-643- US-08-451- US-08-451- US-08-453-0- US-08-155- PCT-US93-0- US-08-480- US-08-643- US-08-643- US-08-476- US-08-476- US-08-476- US-08-378- US-	ID
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29, Applicati 21, Applicati 22, Applicati 23, Applicati 21, Applicati	on
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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Sequence 21, Application Patent No. 5733878 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           | :| ||:: : |||| : | :||| | : | :||| | : | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
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Local Similarity 39.7%;
les 25; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
JENCE 402 AA; 44698 MW; 800499 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 4:
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 6 FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                              21, Application US/08643763A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402 amino acids
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                                                                                                                                                            STANDARD;
                                 US/08643763A
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Pred. No. 5.57e-01;
12; Mismatches 21
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                                                                                                                                                            402 AA
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                                                  APPLICANT:
                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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Query Match 1.8%;
Best Local Similarity 39.7%;
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                                                                                                                         Patent No. 5/4107.
GENERAL INFORMATION:
SMART,
                                                                                                                                                                   Sequence 21, Application US/08451953A Patent No. 5741641
                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: 06-WAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 248-710 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KUBERASAM
APPLICANT: RUBGER, D
APPLICANT: OPPERMANN
APPLICANT: COHEN, CH
APPLICANT: PANG, ROY
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
APPLICANT: COHEN, CHITILE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: FENTON ESq., GILLIAN M. REGISTRATION NUMBER: 36,508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: HOPKINTON
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                                             KUBERASAMPATH, TH
RUEGER, DAVID C.
PANG, ROY H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 SOUTH STREET
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                                                                                             OPPERMANN, HERMA
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                                 COHEN, CHARLES M.
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248-7100
21:
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MORPHOGENIC PROTEIN SCREENING METHOD 33
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Pred. No. 5.57e-01;
12; Mismatches 21
                                                                                 THANGAVEL
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PATENT NO. 5/334.

GENERAL INFORMATION:
COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: KUBERASAMPATH C.
APPLICANT: RUGGER, DAVID C.
APPLICANT: RUGGER, DAVID C.
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Best Local Similarity 39.7%;
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                                                                                                                                                                                                                                                                                               XXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                  194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,953A
FILING DATE: 26-MAY-1995
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NAME: PITCHER ESq., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
JENCE 402 AA; 44764 MW; 803627 CN;
                                                        NUMBER OF SEQUENCES: 3
                                                                               TITLE OF INVENTION: MORPHOGEN TITLE OF INVENTION: ULCERS.
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STATE: M
COUNTRY:
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                                  STREET:
                                             ADDRESSEE:
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5. 5739107
                       HOPKINTON
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                                                                                                     OPPERMANN, HERMANN
PANG, ROY H.L.
OZKAYNAK, ENGIN
SMART, JOHN E.
                                 E: PATENT ADMINISTRATOR,
45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                           TREATMENT OF GASTROINTESTINAL
                                             CREATIVE BIOMOLECULES
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Best Local Similarity 39.7%;
Matches 25; Conservative
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INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                     Sequence 21, Application PC/TUS9308742
                                                                                                                                                                                                                                                                                                                                       XXXXXX
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08742
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 402 AA; 44764 MW; 803627 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERNCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                 TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                COUNTRY: US
ZIP: 01748
                                                                                                                                                                STREET: 45 SOUL
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                    FILING DATE:
                                                                                                                                                       STATE:
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                                                                                                                                             USA
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) 435-6951
~ NO: 21:
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                                                                                                                                                                                                                             MORPHOGEN-INDUCED PERIODONTAL TISSUE REGENERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/445,882
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Pred. No. 5.57e-01;
12; Mismatches 21;
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ATTORNEY/AGENT INFORMATION:
NAME: KELLEY ESQ, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-067

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Best Local S
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08206864
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08206864 Patent No. 5610021
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,070
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841,646
FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 1.8%;
Local Similarity 39.7%;
nes 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/206,864
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7477
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                      APPLICANT: KUBERASAMPATH, THANGAVEL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: RECOMBINANT OSTEOGENIC PROTEIN PRODUCTION
                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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CITY: HOPKINTON
STATE: MA
                                                                                                                                                                                COUNTRY: US
ZIP: 01748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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45 SOUTH STREET
                                                                                                                                                                                           USA
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JONES, WILLIAM K
TUCKER, RONALD F
                                                                                                                                                                                                                                                                                                                       OPPERMANN, HERMA
OZKAYNAK, ENGIN
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Pred. No. 5.57e-01;
12; Mismatches 21
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Best Local Similarity 39.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08155343A
                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/155,343A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESG., GILLLAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067FW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7550
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
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TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein JENCE 402 AA; 44698 MW; 800499 CN;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MORPHOGENIC-I
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: ami
                                                                                                                                                                                                        COUNTRY: USA
ZIP: 01748
                                                                                                                                                                                                                             STATE: MA
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Pred. No. 5.57e-01;
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Best Local :
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Best Local :
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MOLECULE TYPE: protein
SEQUENCE 402 AA; 44764 MW; 803627 CN;
                                                                        TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 402 AA; 44698 MW; 800499 CN;
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       194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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Local Similarity 39.7%;
les 25; Conservation
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                      12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
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                                      Match 1.8%;
Local Similarity 39.7%;
les 25; Conservative
                                                                                                       TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEPAX: 617/248-7100
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                               CITY: HOPKINTON
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                                       Score 125; DB 2; Le
Pred. No. 5.57e-01;
12; Mismatches 21;
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Pred. No. 5.57e-01;
12; Mismatches 21
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                US-07-901-703-11
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US-08-480-528A-8
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194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
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                                                    1.8%;
Local Similarity 39.7%;
les 25; Conservation
                                                                                                                                                                                                     TELEFAX: (617) 248-710
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                             12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                           MOLECULE TYPE: protein 803627 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MA
                                                                                                                                                                        LENGTH: 402 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/480,528A FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 01748
                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
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                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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                                                            Score 125; DB 1; L. Pred. No. 5.57e-01; 12; Mismatches 21;
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STANDARD;

PRT;

402 AA

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Query Match
Best Local Similarity
Matches 25; Conser
             Sequence 29, Application U
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMANN,
APPLICANT: OZKAYNAK, E
                                                                                                                                                           XXXXXX
                                                                                                                                                                                        US-08-147-023-29
                                                                                                 Sequence 29, Application US/08147023
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                               253 SLP 255
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/901,703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OPPERMANN, HERMANN
APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE, 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein SENCE 402 AA; 44698 MW; 800499 CN;
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-057
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ZIP: 02109
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Conservative
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             OPPERMANN, HERMI
OZKAYNAK, ENGIN
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KUBERASAMPATH,
 KUBERASAMPATH, THANGAVEL
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                                                                      US/08147023
                             HERMANN
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Pred. No. 5.57e-01;
12; Mismatches 21; Indels
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 TELEFAX: 617/24
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 579
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 569
FILING DATE: 20-AUG-1990
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 42
APPLICATION NUMBER: US 42
APPLICATION NUMBER: US 42
                                         REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     APPLICATION NUMBER: US 315,342 FILING DATE: 23-FEB-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 6
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61
FILING DATE: 22-FEB-1991
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ADDRESSEE: TESTA, HURWITZ & THIBEAULT
                                                                                   FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                           FILING DATE: 15-AUG-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OSTEOGENIC DEVICES NUMBER OF SEQUENCES: 33
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                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
 TELEPHONE: 61/248-7100
                                                                                                                APPLICATION NUMBER: US 1: FILING DATE: 08-APR-1988
                                                                                                                                                          APPLICATION NUMBER: US 232,630 FILING DATE: 15-AUG-1988
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STATE: MASSAC
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Local Similarity 39.7%;
les 25; Conservative
                                                                  TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
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MOLECULE TYPE: protein
UENCE 402 AA; 44698 MW; 800499 CN;
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY ESQ., MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                   MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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402 AA; 44764 MW; 803627 CN;
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OPPERMANN, HEAL
OZKAYNAK, ENGIN
T: KUBERASAMPATH, THANGAVEL
T"TGER, DAVID C.
                                                          amino acid
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                                                linear
                                                                                                                 (508) 435-9001
                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                              06-MAY-1996
    1.8%; Score 125;
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12; N
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Query Match 1.8%;
Best Local Similarity 39.7%;
Matches 25; Conservative
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                                                 SEQUENCE
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APPLICANT: KUBERAS;
APPLICANT: COHEN,
APPLICANT: OPPERMA
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/406,67:
FILING DATE: 20-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 752,857
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
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                                                                                                                      TELEFAX: (617) 248-71
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                     FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OZKAYI
APPLICANT: RUEGEI
APPLICANT: PANG,
                                               MOLECULE TYPE: protein
ENCE 402 AA; 44764 MW; 803627 CN;
                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: TRANSHMENT TO PREVENT LOSS OF AND/OR
TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         TOPOLOGY:
                                                                                 LENGTH: 402 amino acids
TYPE: amino acid
                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CR
                                                                                                                                                                                             NAME: FENTON ESq., GILLIAN M.
                                                                                                                                                                                                                                APPLICATION NUMBER: US 667,274
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OZKAYNAK, ENGIN
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248-7100
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 Score 125; DB 1; Le
Pred. No. 5.57e-01;
12; Mismatches 21;
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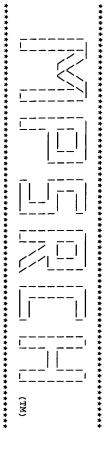
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                                                                            1.8%;
Local Similarity 39.7%;
les 25; Conservation
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                    68 RLP 70
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                         MOLECULE TYPE: protein
JENCE 402 AA; 44698 MW; 800499 CN;
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APPLICANT:
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NAME: FENTON ESG., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-076DV
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: OP3-INDUCED NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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  SLP 255
                                         GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                           FILING DATE: 07-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 01748
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45 SOUTH STREET
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RUEGER, DAVID C.
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                                                                                 Score 125; DB 1; Length 402, Pred. No. 5.57e-01; 12; Mismatches 21; Indels
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RESULT 15
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CC Sequence 21, Applic
CC Patent No. 5650276
CC Patent INFORMATI
CC PAPLICANT: OPP
CC APPLICANT: SMA
CC APPLICANT: COH
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CC CONTENT: END
CC COUNTRY: HOPKIN
CC STATE: MA
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CC TYPE: amino
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                                                                                                        194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR 252
     253 SLP 255
                                                       83
                                                                                                                                         12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS 67
                                                                                                                                                                                                                                       Local
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ENCE 402 AA; 44764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
                                                    RLP 70
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                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                           1.8%;
llarity 39.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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OZKAYNAK, ENGIN
KUBERASAMPATH, TH
RUEGER, DAVID C.
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Pred. No. 5.57e-01;
12; Mismatches 21
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Search completed: Fri Dec 18 18:17:43 1998 Job time: 22 secs.



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:10:34 1998; MasPar time 33.93 Seconds 954.989 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113

1 HASGQRCVLLRTWEALAPAT......PVEDEALGGTAFVQMPAHGL 949

Scoring table: PAM 150 Gap 11

Searched:

107076 seqs, 34141958 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 53.200; Variance 116.643; scale 0.456

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222229887865443221 22222988786554432222222222222222222222222222222222	Result
314 153 153 141 141 146 136 136 137 137 129 129 129 129 129 129 129 129 129 129	Score
	Query Match
115662 3276 4400 3176 3176 3176 3176 3176 3176 3176 3176	Length 1
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hypothetical protein BHLF1 protein - human virion protein homolo hypothetical protein salivary proline-rich protein - hu proline-rich protein homeotic protein - hu proline-rich protein hypothetical protein - hu proline-rich protein hypothetical protein - hu proline-rich protein ORF4 protein - Orf vi proline-rich protein nodulation protein nodulation protein hypothetical protein hypothetical protein prepro osteogenic pro testis-specific prote hypothetical 119.5K p proline-rich protein tumor-associated anti nodulation protein no epithelial tumor anti	Description
1.95e-30 1.03e-05 1.03e-04 2.85e-04 1.65e-03 5.19e-03 1.23e-03 5.19e-03 3.67e-02 1.21e-02 1.2	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
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1.6	1.6	1.6		1.6	1.6	1.6	1.6	•	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.7	1.7
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5.34e-0	8.96e-01	6.93e-01	8.96e-01	8.96e-01	6.93e-01	5.34e-01	6.93e-01	5.34e-01	6.93e-01	6.93e-01	4.12e-01	4.12e-01	5.34e-01	3.17e-01	6.93e-01	1.87e-01	4.83e-02	6.35e-02	2.43e-01	6.35e-02	1.09e-0

ALIGNMENTS

501 QIADRI-KEFKQRILIKKFNNVLPELVFMKFDVKSCYDSIPRMECMR-ILKDALKNENGFF 558 :	Db 501
- PDGLRPIVNMDY-VVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLD 706	Qу 649
	Db 444
	Qy 590
	Db 388
	Оу 530
0 LLKKLRLKDFRWLFIS-DIWFTKHNFENLNQLAIC-FISWLFRQLIPKIIQTFFYCTEIS 387	Db 330
0 LVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNTKKFISLGKHAKLSLQE 529	Qy 470
1 LSHLSRQSPKER-VLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDS 329	Db 271
#gene SGD:EST2 #eross-references SGD:S0004310; MIPS:YLR318w #map_position 12R #MARY #length 884 #molecular-weight 102662 #checksum 7604	#gene #gene #map_ SUMMARY
##residues 1-884 ##label DUZ ##cross-references EMBL:U20618; NID:g2258165; PID:g662136; MIPS:YLR318w ##experimental_source strain S288C (AB972)	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
molecule_type DNA	##
on The sequence S53396	#description
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#accession A03742
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Local Similarity 30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ts annotation; protein coding region
The sequence contains four perfect repeats (residues 149-273, 274-398, 399-523, and 524-648).
TION #superfamily human herpesvirus 4 BHLF1 protein
#length 660 #molecular-weight 66244 #checksum 8900
                                                                                                                                                                                                                                                                                                                                                                                                                         48;
     VIIION #type complete
vIIION protein homolog - bovine herpesvirus 1
alpha TIF; BHV-I protein homolog; ICP25; Vmw65; VP16
#formal_name bovine herpesvirus 1
05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change
09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Glbson, T.J.; Hatfull, G.; Hudson, G.S.; Satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, B.G. Nature (1984) 310:207-211

DNA sequence and expression of the B95-8 Epstein-Barr virus
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Mol. Biol. Med. (1983) 1:21-45
Sequence analysis of the 17,166
Epstein Barr virus.
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BHLF1 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
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S24229
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Pred. No. 6.26e-07;
34; Mismatches 60; Indels
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This protein interacts with cellular transcription factors to transactivate immediate early viral genes.
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##cross-references GB:X78052; NID:g459246; PID:g459248
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Similarity 31.3%;
46; Conservative
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Carpenter, D.E.; Misra, V.
Gene (1992) 119:259-263
Gene (1992) 19:259-263
Sequences of the bovine herpesvirus I homologue of herpes
simplex virus type-1 alpha-trans-inducing factor (UL48).
                                                                                                                                                                                                                                                                                                                                                                                                                                               basic proline-rich protein IB-5; proline-rich peptide #formal_name Homo sapiens #common_name man 19-Feb-1984 #sequence_revision 12-Apr-1996 #text_chang
                                               PIHUSD #type complete salivary proline-rich glycoprotein precursor PRB4 (large allele) - human
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Pred. No. 1.03e-05;
33; Mismatches 56
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Pred. No. 3.83e-04;
23; Mismatches 30;
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#journal Blochemistry (1991) 30:3351-3356
#title Basic proline-rich proteins from human parotid saliva:
    relationships of the covalent structures of ten proteins from a single individual.
#cross-references MUID:91190884
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                                                                                                                                                                                                                                                                                                                                              #title Complete amino acid sequence of a basic proline-rich peptide.
P-D, from human parotid saliva.
#cross-references MUID:83186122
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#journal Genetics (1988) 120:267-278
#title Length polymorphisms in human proline-rich
generated by intragenic unequal crossing
#cross-references MUID:89121440
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##residues 54-57,'E',59-73,'R';82-101 ##label
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##residues 241-310 ##label SAI
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##residues 241-254, 'KN', 257-310 ##label
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$62891
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                             Charlton, A.J.; Baxter, N.J.; Lilley, T.H.; Haslam, E. McDonald, C.J.; Williamson, M.P. FEBS Lett. (1996) 382:289-292
Tannin interactions with a full-length human salivary proline-rich protein display a stronger affinity that single proline-rich repeats.
                                                                                                                                                                                         Shimomura, H.; Kanai, Y.; Sanada, K.
J. Biochem. (1983) 93:857-863
Amino acid sequences of glycopeptides obtained from proline-rich glycoprotein of human parotid saliva.
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J. Biochem. (1983) 93:495-502
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##cross-references GDB:119514;
#map_position 12p13.2-12p13.2
#introns 22/1; 34/1
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#accession B24264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 QLGAATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
                                                                                                                                 y Match 1.9%;
Local Similarity 27.2%;
hes 41; Conservative
                                                                                  24 VNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRP
84 PQGPPPPGGPQQRP-PQGPPPPGGPQPRPPQGPPPPAGPQPPPPAGPHLRPTQG 142
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                                               LGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKR
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Similarity 28.2%;
                                                                                                                                                                                                                                                                                                                                                               Ann, D.K.; Carlson, D.M.
J. Biol. Chem. (1985) 260:15863-15872
The structure and organization of a pi
of a mouse multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B24264 #type fragment
proline-rich protein MP3 - mouse (fragment)
proliname Mus musculus #common_name house mouse
09-Sep-1987 #sequence_revision 09-Sep-1987 #text_c
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                                                                                                                                                                                                                         1-240 ##label ANN
#superfamily proline-r:
#length 240 #checksum
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    predicted
jth 310 #molecular-weight 31351
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protein IB-5
it is unclear from the peptide sequence
a product of the PRB2 (PIR:PIHUPF) or
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#checksum 515
                                                                                                                                 Score 136; DB 2; Le Pred. No. 1.65e-03; 38; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 142; DB 1;
Pred. No. 2.85e-04;
41; Mismatches 52
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                                    16-317
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#accession S160
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                                                                                                                                                                                                                                                                                                    #authors
                                                                                                                                                ##molecule_type DNA
##residues 1-317 ##label ANN
##cross-references GB:M23236; GB:J03891; NID:g200535;
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##residues 1-316 ##label DEG
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Similarity 30.9%;
21; Conservative
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homeotic
                                                                                  #superfamily saliva
                                                                                                                                                                                                                                 Ann, D.K.; Smith, K.; Carlson, D.M.
J. Biol. Chem. (1988) 263:10887-10893
Molecular evolution of the mouse proline-rich protein
multigene family. Insertion of a long interspersed repeated
DNA element.
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                                                                                                                                                                                                                                                                                                                                                  proline-rich protein M14 precursor - mouse
#formal_name Mus muscullus #common_name house mouse
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_c
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deguchi, Y.; Kehrl, J.H.
Nucleic Acids Res. (1991) 19:3742
Nucleotide sequence of a novel die
encodes a DNA binding protein.
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   #length
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            #product proline-rich protein M14 #status predicted #label #label MAT
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Library, January 1991
rfamily unassigned homeobox proteins; homeobox homology
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protein - human
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#molecular-weight 34713
#molecular-weight 31719
                                                                                                 proline-rich
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Pred. No. 1.65e-03;
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#accession S019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##status preliminary
##molecule_type genomic RNA
##residues 1-628 ##label MOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##note
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                                                                                                                                                                          NHAQC-PYGVLLKTHCPLRA-AVTPAAGVCAREKPQGSVAAPEEEDTDPRRL
                                                                                                                                                                                                           SYRHRRPYPLLPNPPAALPSIAYTSSRGKIHHSLPKGALPK-EGAPPPPRRL
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                                                                                                                                                                                                                                                                           SSIRKDALLQTGPRLGHLERLGQPANLRTSERSPPTKRRLPRSSEPNRLPKPLPEATLAP
                                                                                                                                                                                                                                                                                                                 EG-ALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLY-SSGDKEQLRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9%;
Similarity 25.0%;
73; Conservation
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Similarity 26.48;
 S27923
S27923
                                                  $27923  #type complete
gene LF3 protein - human herpesvirus 4
#formal_name human herpesvirus 4, Epstein-Barr virus
19-Mar-1997  #sequence_revision 19-Mar-1997  #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #formal_name turnip yellow mosaic virus
#formal_name turnip yellow mosaic virus, TYMV
21-Nov-1993 #sequence_revision 26-May-1995 #text_change
26-May-1995
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                                  08-Sep-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 137; DB 2; Length 628; Pred. No. 1.23e-03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Mismatches 134;
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Pred. No. 5.19e-03;
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##cross-references GB:M11902; NID:g200544; PID:g200545
CLASSIFICATION #superfamily proline-rich protein
SUMMARY #length 227 #checksum 1378
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title vocal multigene families encoding highly repetitive peptide sequences. Sequence analyses of rat and mouse proline-rich protein cDNAs.

#cross-references MUID:86033799
#contents Clone numbar.
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##cross-references EMBL:M35547; NID:g330420; PID:g330421
# #length 924 #molecular-weight 94304 #checksum
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Local Similarity 27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                            49 QQGPPPPGGPQPRPPQGPPPPGGPQPRP-PQGPPPPGGPQPRPPQGPPPPGGPQQRP-PQ 106
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                                                                                 12
                                                                                                                                                              PPAGPQPRPPQ-GPPPTGPQPRPTQGP-PP 193
                                                                                                                                      HSHPSVGRQHHAGPPSTSRPPRPWDTPCPP 345
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                                                                                                                                                                                                                                                   GPPPPGGPQPRPPQGPPPPGG-PQPRPPQGPPPPGGPQLRPPQGPPPPAGPQPRPPQGPP 165
                                                                                                                                                                                                                                                                                           QLGAATQARPPPHAS-GPRRRLGCE-RAWNHSVREAGVPLGLPAPGARRRGGSASRSLPL 256
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                                                                                                                                                                                                              PKRPRRGAAPEPERTPYGQGSWAHPGRTRGPSDRGFCVVSPAR-PAEEATSLEGALSGTR 315
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Sequence and transcription of Raji Epstein-Barr virus DNA
spanning the B95-8 deletion region.
D34768 #type complete
ORF4 protein - Orf virus (strain NZ2)
#formal_name Orf virus
23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
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#formal_name Mus musculus #common_name house mouse
08-Mar-1989 #sequence_revision 08-Mar-1989 #text_ci
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33; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                               Score 125; DB 2;
Pred. No. 3.67e-02;
34; Mismatches 67
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##cross-references EMBL:X61126
CLASSIFICATION #superfamily proline-rich protein
SUMMARY #length 300 #molecular-weight 31129
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Best Local Similarity 28.2%;
Matches 33; Conservative
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#title
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#journal Virology (1990) 176:379-389
#title Sequence analysis of the inverted terminal repetition in
genome of the parapoxvirus, orf virus.
#cross-references MUID:90266454
#accession D34768
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##cross-references GB:X58438; NID:g53181; PID:g53182
                                                                                                                                                                                                                                                                                            ##molecule_type DNA
##residues 1-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 RAPGRAGRYPAARPAAASAAASRRHRGPAARSSPAAERPAPPRARAEAAAPRRASSS-GS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##residues 1-264 ##label FRA
##cross-references GB:M30023; EMBL:M37623; NID:g332561; PID:g332566
## #ength 264 #molecular-weight 25613 #checksum 1957
      262
                                          187
                                                                                                                   131 PGNQQGPPPQG-GPQQRPP-QPGNQQGPPPPPGGPQQRPPQPGGNQGGPP-QGGPHP-PPR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 RASSGPPRRSAARS-SAASGSRPAASGPAARAPAASSARTSAGEGAARGPGAPRAGW 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 RAWNHSVR-EAGVPLGLPAPGARRRGGSASRSLPLPKRP---R-RGAAPEPERTPVGQGS 277
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                                                                                                                                                1.8%;
Local Similarity 25.2%;
les 34; Conservation
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                                    PGNQQGPPPQGGPQQRPTQPGNQQGPPQQGG-PQAPPRPGNQQGPPPQGPQGPPRTGNQQ 245
    RGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPARPA-EEATSLEGALSGTRHSHPS 320
                                                                               AATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPR 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #type complete
proline-rich protein MP4 - mouse
#formal_name Mus musculus #common_name house
22-Nov-1993 #sequence_revision 10-Nov-1995 #t
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Gene sequence of mouse B-type proline-rich protein MP4.
Transcriptional start point and an upstream phylogenetic footprint with ets-like and rel/NFkB-like elements.
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Pred. No. 1.21e-02;
40; Mismatches 37
                                                                                                                                                            40;
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Pred. No. 6.89e-03;
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Matches 3
Query Match 1.8%;
Best Local Similarity 30.4%;
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#journal
#title
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#journal Mol. Microbiol. (1990) 4:921-932
#title Analysis of three nodD genes in Rhizobium leguminosarum
biovar phaseoli; nodD1 is preceded by nolE, a gene who
product is secreted from the cytoplasm.
#cross-references MUID:91014692
#accession S11790
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#accession $10889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                              #residues 1-309 ##label LYO
#cross-references EMBL:X07881; NID:g35637; PID:g296669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 AFRALVAQCLVCVPWDA-RPPPAAPSFRQVSCLKELVARVL-QRLCERGAKNVLAFGFAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIRTWEALAPATP-AMPRAPRCRAVRSLLRSHYREVLPLATFVRRIGPQGWRLYQRGDPA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMIERNLTAAARSINLSQPAMSAAVRRL-RSYFRDEL-FTMRGREFVPTP-R-AEDLAPA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 1.8%;
Similarity 31.4%;
38; Conservative
                                                     22/1; 34/1
#superfamily proline-rich protein
#length 309 #molecular-weight 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #superfamily regulatory protein lysR DNA binding; transcription regulation #length 302 #molecular-weight 34274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #formal_name Rhizobium leguminosarum bv. phaseoli
21-Nov-1993 #sequence_revision 13-Jan-1995 #text_change
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S11790 #type complete nodulation protein nodD3 - Rhizobium leguminosarum phaseoli
                                                                                                                                                                                                                                                Lyons, K.M.; Stein, J.H.; Smithles, O. Genetics (1988) 120:267-278
Length polymorphisms in human proline-rich protein genes generated by intragenic unequal crossing over.
                                                                                                                                                                                                                                                                                                                                                                                  $10889 #type complete
proline-rich protein - human
proline-rich protein - human
formal_name Homo sapiens #common_name man
07.oct-1994 #sequence_revision 26-May-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nodD3
                                                                                                                                                                                                                                                                                                                                                                 08-Sep-1997
                                                                                                                                                                                          preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-302 ##label DAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not compared with conceptual translation
Score 129; DB 2;
Pred. No. 1.21e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 126; DB 2; Length 302; Pred. No. 2.79e-02; 28; Mismatches 46; Indels
                                                       30936 #checksum
               Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
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                                                                                                        176
 311 LSGTRHSHPSVGRQHHAGPPSTSRPPRP 338
                                                                    254 LPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRG-F-CVVSPARPAE-EATSLEGA 310
                                                                                                                                        194 GPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRS
                                                                                                                                                                    122 GPPP-QGGNQSQG-PPPHPGKPEGPPP-QGG-NQSQGPPPRP-GKPE-GPPPQGGNQSQG 175
                                  -NKPRGPPPHPGKPQGPPPQEGNKPQRP 260
                                                                                                    -P-PPRPGKPEGPPPQGGNQSQGPPPRPGKPEGPPPQGGNQSQGPPPRPGKPEGSPSQGG 233
                                                                                                                                                                                                          45;
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                          38;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                          53;
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                                                                                                                                                                                                          12;
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Search completed: Fri Job time : 109 secs.

Dec

18 18:12:23 1998

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Dec 18 18:12:41 1998; MasPar time 25.51 Seconds 998.601 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-951-733-14 (1-949) from US08951733.pep (1 of 2) 7113

1 HASGQRCVLLRTWEALAPAT.....PVEDEALGGTAFVQMPAHGL 949

Scoring table: PAM 150 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swissprot

Statistics: Mean 54.986; Variance 96.850; scale 0.568

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2222218 322222223	Result
162 153 142 142 143 133 133 137 125 125 125 127 1218 1118 1118 1118 1118 1118 1118	Score
111111111111111222	Query Match I
566 276 276 276 276 276 276 276 276 277 277	Length [
	B
YHL1_EBV ATIN_HSVBP PAREL_HUMAN PRPL_HUMAN PRP2_MOUSE PRP3_MOUSE PRP3_MOUSE NOD1_RHISN MFH1_HUMAN MFH1_HUMAN MFH2_HOWAN M	IJ
HYPOTHETICAL BHLF1 PRO ALPHA TRANS-INDUCING P SALIVARY PROLINE-RICH SALIVARY PROLINE-RICH SALIVARY PROLINE-RICH 69 KD PROTEIN PROLINE-RICH PROTEIN M PROLINE-RICH PROTEIN M NODULATION PROTEIN D I BONE MORPHOGENETIC PRO MESENCHYME FORK HEAD D TESTIS-SPECIFIC PROTEIN D I BONE MORPHOGENETIC PRO MESUNCHATION PROTEIN D I BONE MORPHOGENETIC PRO MESUNCHATION PROTEIN D REGULATION PROTEIN E2. HYPOTHETICAL GENE 1 PR TRNA-(MS[2]10[6]A)-HYD HYPOTHETICAL GENE 1 PR TRNA-(MS[2]10[6]A)-HYD NODULATION PROTEIN D I SALIVARY PROLINE-RICH G1/S-SPECIFIC CYCLIN E G1/S-SPECIFIC CYCLIN E	Description
4.85e-09 4.48e-07 4.48e-07 8.26e-06 1.97e-04 4.98e-05 2.95e-03 3.91e-04 2.95e-03 2.95e-03 2.95e-03 2.95e-03 2.95e-03 2.95e-02 2.87e-02 2.87e-02 2.87e-02 2.87e-02 1.01e-01 1.01e-01 1.01e-01	Pred. No.

44 45	4 2 3	41	40	39	38	37	36	35	34	3 3	32	31	30	29	28	27	26	25	24
105 105	108 105	110	107	107	110	109	107	109	106	106	107	115	113	114	113	112	113	111	111
1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.5	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6
890 2774	706 863	628	529	494	408	324	318	301	285	233	174	3149	1255	705	704	633	514	509	498
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ACO1_ECOLI MAPA_RAT	SYN1_BOVIN HIS2_NEUCR	V70K_TYMVC	DNB2_ADE05	MFH1_MOUSE	CGE3_XENLA	MATD_NEUCR	NODD_RHILT	NDO3_RHILO	YAFY_ECOLI	YFJR_ECOLI	BAR1_CHITE	TEGU_EBV	MUC1_HUMAN	SYN1_HUMAN	SYN1_RAT	LA17_YEAST	VE2_HPV5B	VE2_HPV36	VE2_HPV08
ACONITATE HYDRATASE 1 MICROTUBULE-ASSOCIATED	SYNAPSINS IA AND IB. PHOSPHORIBOSYL-AMP CYC	69 KD PROTEIN.	EARLY E2A DNA-BINDING	MESENCHYME FORK HEAD P	G1/S-SPECIFIC CYCLIN E	MATING TYPE PROTEIN A-	NODULATION PROTEIN D.	NODULATION PROTEIN D3.	HYPOTHETICAL TRANSCRIP	HYPOTHETICAL TRANSCRIP	BALBIANI RING PROTEIN	LARGE TEGUMENT PROTEIN	MUCIN 1 PRECURSOR (POL	SYNAPSINS IA AND IB (B	SYNAPSINS IA AND IB.	PROLINE-RICH PROTEIN L	REGULATORY PROTEIN E2.	REGULATORY PROTEIN E2.	REGULATORY PROTEIN E2.
1.49e+00 1.49e+00	6.20e-01 1.49e+00	3.41e-01	8.32e-01	8.32e-01	3.41e-01	4.60e-01	8.32e-01	4.60e-01	1.11e+00	1.11e+00	8.32e-01	7.38e-02	1.37e-01	1.01e-01	1.37e-01	1.86e-01	1.37e-01	2.52e-01	2.52e-01

ALIGNMENTS

RESULT ID A AC P DT 0	Qy Db	о Оу	Qy Db	Qu Be	SQ	FΤ	FΤ	ΨT	ΤΉ	FΤ	ΚW	DR	DR	RĽ	RA	RA :	RA.	RX	RP :	R C	86	2 2	ijij	Ŋ	ΡŢ	Å	Ħ	RESULT
T 2 ATIN_HSVBP STANDARD; PRT; 504 AA. P30020; O1-APR-1993 (REL. 25, CREATED)	365 QDLAAAQRC-PAGPPPTRSGA-AAQRTHR-RPPGCP 397 :::1: : :: : : 309 GALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCP 344	307 TGGRPAAPGAPGTPAAPGPGGGAAVPSGATPHPERGSGPADPPAAARLPPERGEPRLP 364 :: : :: :	251 GPPPTRSGAAAQ-RTHRRPPGCPRSARNPGCPRTWRRR-SGAQRGHPPPGAGQRPSGP 306 : : :: :	Query Match 2.3%; Score 162; DB 1; Length 660; Best Local Similarity 30.8%; Pred. No. 4.85e-09; Matches 48; Conservative 34; Mismatches 60; Indels 14; Gaps 12;	CE 660 AA;		399 523	274 398	149 273 1.	149 648 4 X 125		403742; C	EMBL; V01555; -; NOT_ANNOTATED_CDS.	10:207		ON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN			SEQUENCE FROM N.A.		VIRIDAE: DS-DNA ENVELOPED VIRUSES: HERPESVIRIDAE: GAMMAHERPESVIRINAE.	PROTEIN.	(REL.	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)	(REL.	91;	HT1	IT 1

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RESULT

AC PH

A
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Matches 4
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Best Local (
     Matches
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01-MAR-1989 (REL. 10, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) (CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: RESPONSIBLE FOR TRANSCRIPTIONAL ACTIVATION OF EARLY PROMOTERS (ALPHA GENES) (BY SIMILARITY).
-!- SIMILARITY: TO OTHER HERPESVIRUSES ALPHA TRANS-INDUCING EMBL; Z11610; E264419; -.
PIR; S24229; S24229.
PIR; JC1306; JC1306.
TRANSCRIPTION REGULATION; TRANS-ACTING FACTOR; DNA-BINDING. SEQUENCE 504 AA; 54028 MW; 79F42020 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).
BOVINE HERPESVIRUS TYPE 1 (STRAIN P8-2).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRI
                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SMI
GENETICS 120:255-265(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARPENTER D.E., MISRA V.;
GENE 119:259-263(1992).
                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 89121439.
                                                                                                                                                                                                                                                                                                                                               SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRPM_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 93012995.
                                                                                                                                              NON_TER
                                                                                                                                                                          REPEAT; PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 165-234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 APAEAGGGWRRSGSTRTRGRAARSTTGRLQRPCCGPRRRAKC-CRATP-RQRLR--ARGE 406
                           Local Similarity
                                                                                                                                                                                                                                                                 x07704; E265547; -.

A03295; PIHUSD.

S03175; S03175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QHHAGPPSTSRPPRPWDTPCPPVYAET 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPACGGPSRARGGRRRASPANP-FGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERTPYGQGSWAHPGRTRGPSDR-GF-CVV-S-PARPAEEATSLEGALSGTRHSHPSYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRHTS-GSGAFSQ-GRRPGRVCRLGWACKARSGPARGGPGPSPVRSGLGLSR-ARGSPGP 463
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                                                                                                                                                                                                                                                P19999; 1CLG
  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 2.2%;
Similarity 31.3%;
46; Conservative
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                                                                                                 165
234 /
     Conservative
                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                           2.1%;
29.3%;
                                                                                                 234
23676
                                                                                                                                                                       SALIVA; MULTIGENE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMITHIES
                                                                                                 , WM
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VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
Score 150; DB 1;
Pred. No. 4.48e-07;
41; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 153; DB 1; L
Pred. No. 1.47e-07;
33; Mismatches 56;
                                                                                                 PEPTIDE P-D.
; ED2D4ADC C:
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                                                                                                 CRC32;
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     53;
                                                  Length 234;
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  Indels
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     10;
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  Gaps
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RESULT PER COLOR PROCESSES COL
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 4
                                                        PRPA_HUMAN STANDAKU;
P10163; P02813;
P1-JUL-1986 (REL. 01, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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p10162; p03813;
01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS: PEPTIDE P-D)
  HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X07715; E4806; ALT_SEQ.
PIR; A03295; PIHUSD.
PIR; S03176; S03176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT; PAROTID GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAITOH E., ISEMURA S., SANADA
J. BIOCHEM. 93:495-502(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 89121439.
LYONS K.M., STEIN J.H., SM
GENETICS 120:255-265(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG-P-PP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPPGGNPQQPQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPPP-QGGNQSQG-PPPHPGKPERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG 141
                                                                                                                                                                                                                                                                                                                                      SHPSVGRQHHAGPPSTSRPPRP
                                                                                                                                                                                                                                                                                                                                                                                         APPAGKPQGPPPPPQGGRPPRP 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAE-EATSLEGALSGTRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 2.0%;
Similarity 28.2%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF 207-276.
83186122.
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276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27816 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 142; DB 1;
Pred. No. 8.26e-06;
                                                                                                                                                                                                                                                                                                                                         338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE P-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276
                                                                                     (ALLELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 276;
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                                                                                     S)
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Best Local S
Matches 4
                                                                                                          Query Match
Best Local
                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYONS K.M., STEIN J.H., SMITH GENERICS 120:267-278(1988).
EMBL; KOO3207; G190508; -.
EMBL; XO7882; G296670; -.
HSSP; P19999; 1CLG.
MIM; 168730; -.
MIM; 180990; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         V70K_TYMV
P10357;
                                                                                                                                           MORCH M.D., BOYER J.C., HAENNI A.L.;
NUCLEIC ACIDS RES. 16:6157-6173(1988).

-!- FUNCTION: NOT KNOWN.
-!- SIMILARITY: TO 65 TO 70 KD PROTEIN FROM OTHER TYMOVIRUSES.
EMBL; X07441; G62223; ALT_SEQ.
PIR; S01955; S01955.
SEQUENCE 628 AA; 69195 MW; 9E64ED49 CRC32;
                                                                                                                                                                                                                                                                                                  01-MAR-1989 (REL. 10, CREATED)
01-AUG-1992 (REL. 23, LAST SEQ
01-AUG-1992 (REL. 23, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAEDA N.,
                                                                                                                                                                                                                                                                TURNIP YELLOW MOSAIC VIRUS.
VIRIDAE; SS-RNA NONENVELOPED VIRUSES; TYMOVIRIDAE
                                                                                                                                                                                                                                                                                        69 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155
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                                                                       157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   255
  250
                         215
                                               194
                                                                                                                                                                                                                            EQUENCE FROM N.A. EDLINE; 88289359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102
                                                                                            1.9%;
Local Similarity 25.0%;
ses 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 40; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDA N., KIM H.-S., AZEN E.A., SMITHIES BIOL. CHEM. 260:11123-11130(1985).
                                                                                                                                                                                                                                                                                                                                                                                                    TRHSHPSVGRQH-HAGPPSTSRPPRP 338
                       VRRPLLAPNQFHSPRQPPPLSDDPGILGPRPLAPHSTRDPPPRPI-TPGPSN-THDLRPL 272
                                                                      GPVLTETKPRTSVROPRSATRGPSFRPILLPKV-VH-VHDDPPHSSLRPRGSRSRQLQPT 214
                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                         QQPQDPPAGKPQGPPPPPQGGRPPRP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDR-GFCVVSPARPAEEATSLEGALSG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PPHPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPPGKPQGPPPAGGNP 213
 ASRSLPLPKRPRRGAAPEPERTPVG-QGSWA-HPGRTRGPSDRGFCVVSPARPAEEATSL
                                               PPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPP-QGGNQSQGTPPPPGK-PERPPP-QGG-NQSHRPPPPP-GKPER-PPPQGGNQSQG- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PAROTID GLAND; 1
1 16
17 39
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247 AA;
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larity 27.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40
37
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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25108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MULTIGENE FAMILY; SALIVA; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMITHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                     SEQUENCE U
                                                                                            Score 137; DB 1;
Pred. No. 4.88e-05;
64; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 133; DB 1; Length 247; Pred. No. 1.97e-04; 40; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCOSYLATED PROTEIN A MISSING (IN REF. 2).
D -> A (IN REF. 2).
D -> B (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                               Mismatches 134;
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                                                                                                                                                                                                                                                                                                   ON UPDATE)
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                                                                                                                   Length 628;
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                                                                                               Indels
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RESOLT IN RESOLT IN RESOLT IN RESOLT IN RESOLT IN RESOLT IN RESOLT IN RESOLT IN RESOLT IN RESOLUTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
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Best Local Similarity 27.0%;
                                                                                                                                                                                                                                                                                                                   P05143;
P05143;
13-AUG-1987 (REL. 05, C.
13-AUG-1987 (REL. 05, L.
01-OCT-1994 (REL. 30, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                     PRP.
MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA;
                                             SEQUENCE FROM N.A.
MEDLINE; 86059475.
ANN D.K., CARLSON D.M.;
ANN BIOL. CHEM. 260:15863-15872(1985).
EMBL; M12100; G200549; -.
HSSP; P19999; 1CLG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANN D.K., CARLSON D.M.;
J. BIOL. CHEM. 260:15863-15872(1985).
EMBL; M12099; G200547; -
HSSP; P19999; ICLG.
REPEAT; SALIVA; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRP.
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13-AUG-1987 (REL. 05, LAST SEQUENCE UF
01-CCT-1994 (REL. 30, LAST ANNOTATION
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                   EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRP3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                             REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 86059475.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L3-AUG-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 GGPQQQPPQGPPPPGGPQPRPPQGPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 PPPPGGPQLRPPQGPPPPAGP-QPRPPQGPPPPAGPQPRPPQGPPTTGPQPRPTQGPPPT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 ATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 VGRQHHA--GPPSTSRP-PRPWDTPCPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 PPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQQRPPQGPPPPGGPQPRPPQG 135
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  SALIVA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                              05, CREATED)
05, LAST SEQUENCE UPDATE)
30, LAST ANNOTATION UPDAT
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26034 MW;
                                                                                                                                                                                                                                                                                                                                      MP-3 (FRAGMENT).
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Pred. No. 2.95e-03
33; Mismatches 6
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PROLINE-RICH PROTEIN MP-2.

9D830DAF CRC32;
                                                                                                                                                                                                                                                           VERTEBRATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
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Best Local S
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Best Local
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BMP8_HUMAN
P34820;
01-FEB-1994
01-FEB-1994
15-JUL-1998
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DAVIS E.O., JOHNSTON A.W.B.;
MOL. MICROBIOL, 4:921-932(1990).

MOL. MICROBIOL, 4:921-932(1990).

MOL. MICROBIOL, 4:921-932(1990).

WHICH ENCODE REGULATES THE EXPRESSION OF THE NOD ABCFE GENES
WHICH ENCODE OTHER NODULATION PROTEINS. NODD IS ALSO A NEGATIVE
REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONOIDS AS INDUCERS.

REGULATOR OF THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S11790; S11790.

PROSITE; PS00044; HTH_LYSR_FAMILY; 1.

NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPRESSOR; PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHIZOBIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLI). PLASMID SYM.
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01-NOV-1991 (REL.
01-NOV-1995 (REL.
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P23720;
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                                                                                                                                                                                                                                                                             AFRALVAQCLVCVPWDA-RPPPPAAPSFRQVSCLKELVARVL
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                                                                                                                                                                                                                                                                                                                          IREALQHIRLNIIPWDKFTPDQSDRHFR-VS-LCDFVTVVLFQKILERLAREAPGISFDL 130
                                                                                                                                                                                                                                                                                                                                                                     LLRTWEALAPATP-AMPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPQGWRLVQRGDPA
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larity 31.4%;
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larity 26.4%;
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                                                                                              STANDARD;
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    36,
28,
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34274 MW;
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LAST ANNOTATION UPDATE)
CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 3
38; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 126; DB 1;
Pred. No. 2.12e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H-T-H MOTIF (BY SIMILARITY).
; ED62D2FA CRC32;
                                                                                              PRT;
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d. No. 3.91e-04;
Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT AC OBSESSION OF THE SULT ACCORDANCE OF
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CARBOHYD
CARBOHYD
                                                                                     MFH1_HUMAN STANDARD; PRT; 501 AA. 099558; 0799558; 0799558; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 0799569; 079956
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-!- SIMILARITY: BELONGS TO THE
EMBL; M97016; G189390; -.
PIR; A45056; A45056.
HSSP; P08112; 1TFG.
                                                                                                                                                                                                                                                                                                                                                                                         FKHL14 OR PLANT HUMAN).
HOMO SAPIENS (HUMAN).
CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OEZRAYNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,
WARREN F.D., DRIER E.A., OPPERMANN H.;
J. BIOL. CHEM. 267:2520-25227(1992).
-i- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
AND BONE HOMEOSTASIS (BY SIMILARITY).
                                  EMBL; Y08223
MIM; 602402;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 97312712.
                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FKH-14).
FKHL14 OR MFH1.
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EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-HIPPOCAMPUS;
MEDLINE; 93094231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BONE MORPHOGENETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 SLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 GPPLYQLGAATQA-RPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GLALCALGGGGPGLRPPP-GC-PQRRLG-ARERRDVQREILAVLGLPGR-PRPRAPPAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 RLP 70
                                                         Y08223; E303016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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   PS00657; FORK_HEAD_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00250; TGF_BETA;
                                                                                                                                                                                                                                                                                                                                                                            PRIMATES.
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263
402
367
399
401
158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOKINE; BONE; CARTILAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE-LINKED.
TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 2.95e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8F20C81B CRC32;
                                                                                                                                                                                           IN THE FORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                      TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TETRAPODA;
                                                                                                                                                                                                                                                    SUGIYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 402
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                                                                                                                                                                  Matches
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Q01755;
Q1-NOV-1995
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDAT
TESTIS-SPECIFIC PROTEIN PBS13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
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DEVELOPMENT 111:561-571(1991).
-i- FUNCTION: POSSIBLY PLAYS AN IMPORTANT AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTION DNA_BIND
                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X52128; G54853; -. PIR; S22933; S22933. MGD; MGI:98544; TCP11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY:
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MEDLINE; 91372153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                 DOMAIN
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    295
                                                                                  239
                                        94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPERMATOCYTE STAGE.
SIMILARITY: SOME TO YEAST SOK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: TESTIS.

DEVELOPMENTAL STAGE: FIRSTLY EXPRESSED
                                                                              SARGIDRYGSTVARARPPSPQGPRRGAVKTAPRGPYGHGGLRIGPTSRCPQPSARAKLPS 93
| | | | | | : : | : | | | | | | | : : | | | | | | : :
PAPGARRRGGSASRSLPL-PKRPRRGAAPEPERTPYGQGS-WAHP-GRIRGPSDRG-FCV 294
                                        VTRGAPLPPSPG-KGHLGGTPSSH 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSSGDKEQLRPSFLLSSLRPSLTGARRLVETIFLG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHSGDLNHL-PGHTFAAQQQTFPNVREMFNSHRLG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPARPAEEATSLEGALSGTRHSHPSVGRQH-HAGPPSTSRPPRPWDTPCPPVYAETKHFL 354
  VSPARPAEEATSLEGALSGTRHSH
                                                                                                                                                                                                                                                                                   ; SPERMATOGENESIS; 1
171 206
276 318
419 432
440 509
298 318
298 304
305 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%;
Similarity 28.4%;
27; Conservat'
                                                                                                                                                                                     1.8%;
Similarity 35.7%;
                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
387
397
400
416
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATION;
                                                                                                                                                                                                                                                   ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FORK_HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORK_HEAD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53719 MW;
                                                                                                                                                                                                                                                 61970 MW;
                                                                                                                                                                                                                                             S; REPEAT; COILED COIL.

COILED COIL (8 HEPTADS).

COILED COIL (8 HEPTADS).

COILED COIL (10 HEPTADS).

COILED COIL (10 HEPTADS).

LEUCINE-RICH REPEATS.

LER 1.

LRR 2.

LRR 3.

LRR 3.

LRR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 125; DB 1;
Pred. No. 2.95e-03;
                                                                                                                                                                  19;
                                                                                                                                                                                     Score 127;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORK-HEAD.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALA/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99D32EFA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPDATE
                                                                                                                                                                                     DB 1;
1.51e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEAR PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.P., RUDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                  30;
                                                                                                                                                                                                         Length 566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACHYTENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPERM DEVELOPMENT
                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,
                                                                                                                                                                  5
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM8A_MOUSE P34821;
                                            MEDLINE; 93094231.

MEDLINE; 93094231.

OEZKARNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,

OEZKARNAK E., SCHNEGELSBERG P.N.J., JIN D.F., CLIFFORD G.M.,

WARREN F.D., DRIER E.A., OPPERWANN H.;

J. BIOL. CHEM. 267:25220-25227(1992).

-i- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE

OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF

EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION

AND BONE HOMEOSTASIS (BY SIMILARITY).

-i- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.

-i- DEVELOPMENTAL STAGE: EXTENSIVE EXPRESSION FOUND IN 8-DAY EMBRYOS,

FELL DRASTICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN 17-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQ
01-CCT-1996 (REL. 34, LAST ANN
BONE MORPHOGENETIC PROTEIN 8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: AE000065; G2182301; --
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
NODULATION; TRANSCRIPTION REGULATION; DNA-BINDING; ACTIVA
REPRESSOR; MULTIGENE FAMILY; PLASMID.
DNA_BIND
23
42
H-T-H_MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHIZOBIUM SP. (STRAIN NGR234).
PLASMID SYM PNGR234A.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
NODULATION PROTEIN D I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOD1_RHISN P55359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMP6A OR BMP8 OR BMP-8.
MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 97305956.
FREIBERG C.A., FELLAY R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -11 FUNCTION: NODD REGULATES THE EXPRESSION OF THE NOD ABCFE GENES WHICH ENCODE OTHER NODULATION PROTEINS. NODD IS ALSO A NEGATIVE REGULATOR OF ITS OWN EXPRESSION. BINDS FLAVONDIS AS INDUCERS.
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NATURE 387:394-401(1997).
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                                                                                                                                                                                                                                                                                                                                                                                TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHIZOBIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 -II-LSDFMTLMFLERVVVRVAREAPAVSFELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 LRTYFRDEL-FTMNGRELVPTP-R-AEALAPAVREALLHIHLSIISWDPFNPAQSDRSFR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 QVSCLKELVARV-LQRLCERGAKNVLAFGFALL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OP-
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRSHYREVLPLATEVRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDA-RPPPAAPSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
28; Conse
                                EMBRYOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%;
larity 30.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHORDATA;
TO THE TGF-BETA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAIROCH A., BROUGHTON W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE UPDATE)
ANNOTATION UPDATE)
8A PRECURSOR (BMP-8A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 121; DB 1; L
Pred. No. 1.09e-02;
23; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FA5238EE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-BINDING; ACTIVATOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OSTEOGENIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSENTHAL A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 2
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Best Local Similarity 38.7%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UL61_HCMVA
P16818;
01-AUG-1990
01-AUG-1990
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 90269039.

CHEE M.S., BANKIER A.T., BECK S., BOHNI R., BROWN C.M., CERNY R.,

HORSNELL T., HUTCHISON C.A. III, KOUZARIDES T., MARTIGNETTI J.A.,

HORSNELL T., HUTCHISON C.A. TOMLINSON P., WESTON K.M., BARRELL B.G.;

CURR. TOP. MICROBIOL. IMMUNOL. 154:125-169(1990).

EMBL; X17403; E27260; -.

PIR; S09824; S09824.

HYPOTHETICAL PROTEIN.

SEQUENCE 431 AA; 44309 MW; 232AB9D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
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CHAIN
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MGD; MGI:104515; BMB8A.
PROSITE; PS00250; TGF_BETA;
SIGNAL; GROWTH FACTOR; CYTOR
SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN CYTOMEGALOVIRUS (STRAIN AD169).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; BETAHERPESVIRINAE.
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325 TAPDGAPGRWDGPADGPAPGLGRG 348
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270 RTPVG-QGSWAHPGRTRGPS-DRG 291
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                                                                                                                                                                                                                                                                                                         y Match 1.7%;
Local Similarity 32.1%;
hes 27; Conservative
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                                                                                                                                                        HASGPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSAS-RSLPLPKRPRRGAAPEPE 269
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298
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AA;
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(REL. 15, LAST SEQUENCE UPDATE)
(REL. 17, LAST ANNOTATION UPDATE)
L PROTEIN UL61.
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                                                                                                                                                                                                                                                                                                         Score 118; DB 1; Length 431 Pred. No. 2.87e-02; 20; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
BONE MORPHOGENETIC P
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 2.87e-02;
12; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
7075AleD CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 399;
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Search completed: Fri Dec Job time : 79 secs.

18 18:14:00 1998

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(MT)	

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Fri Dec 18 18:37:59 1998; MasPar time 18.72 Seconds 800.790 Million cell updates/sec

Description: Perfect Score: >US-08-951-733-14 (640-940) from US08951733.pep (2 of 2) 2214

Sequence: TSRLRFIPKPDGLRPIVNMD......NLRKTVVNFPVEDEALGGTA 301

Scoring table: PAM 150 Gap 11

Searched: 165420 segs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 47.179; Variance 86.093; scale 0.548

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
2214 1596 1597 375 375 201 108 108 108 108 109 100 100 100 100 100 100 100 100 100	Score
1000 1000 1000 1000 1000 1000 1000 100	Query Match Length
1132 1132 1132 988 989 1031 884 366 561 1002 3410 280 3410 3410 3410 3410 3410 3410 3410 341	Length 1
444888888888888888888888888888888888888	80
014746 0104783 070372 013338 0010939 0013338 00151242 025293 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529 04529	Ħ
	! !
TELOMERASE REVERSE TRA TELOMERASE CATALYTIC S TELOMERASE REVERSE TRA TELOMERASE SUBUNIT PL2 CHROMOSOME XII COSMID HYPOTHETICAL 10.7 KD P GTP-BINDING PROTEIN (G DY3.4. NITRITE REDUCTASE (NAD FLAVONOID 3',5'-HYDROX POLYPROTEIN PRECURSOR. POLYPROTEIN PRECURSOR. POLYPROTEIN PRECURSOR. YAFJ. HYPOTHETICAL PROTEIN M ORF (FRAGMENT). MATURASE-RELATED PROTE NEUROFILAMENT-LIKE PRO NYPOTHETICAL 66.2 KD P	Description
0.00e+00 0.00e+00 0.00e+00 3.34e-52 3.34e-52 1.10e-08 6.37e-02 2.29e-01 2.29e-01 2.29e-01 5.85e-01 1.08e+00 1.0	Pred. No.

45	44	43	42	41	40	39	38	37	36	35 5	34	33 33	32	31	30	29	28	27	26	25	24	23	22	21
94	93	93	93	93	94	94	95	95	95	96	96	96	96	95	95	96	96	95	96	96	97	97	97	99
4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.3	4.3	4.3	ω	4.3	4.3	4.3	<u>4</u> ۵.	4 .3	4.3	4.3	<u>4</u> 3	4.3	4.3	4.4	4.4	4.4	
2910	802	581	528	368	364	314	3411	3410	3410	1216	786	899	625	575	363	363	308	307	286	245	1398	358	275	1176
v	10	N	10	N	13	σı	14	14	14	11	œ	G	G	ω	13	14	N	N	14	\vdash	ب	10	σ	ω
Q26008	P93042	051662	Q41592	067880	012975	001873	Q98803	Q89278	Q89277	Q62884	Q34832	Q94607	044733	036013	057518	Q69275	P96605	033708	039304	059069	P72186	065581	045575	Q08236
RNA POLYMERASE I.	ROOT HAIR DEFECTIVE 3.	THREONYL-TRNA SYNTHETA	WPK4 PROTEIN KINASE.	GLUCOSYL TRANSFERASE I	ALDOLASE.	SIMILAR TO CUTICULAR C	POLYPROTEIN.	POLYPROTEIN.	POLYPROTEIN.	VASCULAR PROTEIN TYROS	INTRON ORF.	JUVENILE HORMONE BINDI	F54D7.1 PROTEIN.	HYPOTHETICAL PROTEIN C	FRUCTOSE-1,6-BISPHOSPH	PROTEIN KINASE; GLYCOP	PROBABLE TRANSPORT ATP	THYMIDINE DIPHOSPHO-4-	NO COUNTERPARTS IN HSV	245AA LONG HYPOTHETICA	PYROLYSIN.	FRUCTOSE-BISPHOSPHATE	F56A8.4.	CHROMOSOME XV READING
4.81e+00	6.44e+00	6.44e+00	6.44e+00	6.44e+00	4.81e+00	4.81e+00	3.59e+00	3.59e+00	3.59e+00	2.67e+00	2.67e+00	2.67e+00	2.67e+00	3.59e+00	3.59e+00	2.67e+00	2.67e+00	3.59e+00	2.67e+00	2.67e+00	1.98e+00	1.98e+00	1.98e+00	1.08e+00

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ALIGNMENTS

용	Qy Db	Qy Db	Оу	g g	X A O	RA R	7 F F 7	3885	Brade	RESULT
858 RRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT 917	798 LNEASSGLEDVFLREMCHHAVRIRGKSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGI 857 	738 TYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSS 797 	678 ASYLGLDDIHRAWRTFYLRYRAQDPPPELYFYKYDYTGAYDTIPQDRLTEYIASIIKPQN 737 	618 TSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLG 677 	Query Match 100.0%; Score 2214; DB 4; Length 1132; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MEDLINE; 97400623. NAKAMURA T.M., WORIN G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H., LINGNER J., HARLEY C.B., CECH T.R.; SCIENCE 277.955-959(1997). EMBL; AF015950; G2330017; RNA-DIRECTED DNA POLYMERASE. SEQUENCE 1132 AA; 126995 MW; 2DFBEDF3 CRC32;	[1] SEQUENCE FROM N.A. TISSUE-KIDNEY;	HTMT. HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHEDTA: DETMATES	., 1998 (TREMBLREL. 05, CREATED) 1998 (TREMBLREL. 05, LAST SEC 1998 (TREMBLREL. 06, LAST AN NASE REVERSE TRANSCRIPTASE.	LT 1 O14746 PRELIMINARY; PRT; 1132 AA.

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014783;
                                                                                                                                                                             O70372 PRELIMINARY; PRT; 1122 AA.
O70372;
O1-AUG-1998 (TREMBLREL. 07, CREATED)
O1-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TELOMERASE REVERSE TRANSCRIPTASE.
MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEYERSON M., COUNTER C.M., EATON E.N.,
CADDLE S.D., ZIAUGRA L., BEIJERSBERGEN
BACCHETTI S., HABER D.A., WEINBERG R.A.
CELL 90:785-795(1997).
EMBL; AF018167; G2347129; -.
SEQUENCE 1132 AA; 126937 MW; C1E5E2
                     GREENBERG R.A., ALLSOPP R. ONCOGENE 0:0-0(1998). EMBL; AF051911; G3005592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
TELOMERASE CATALYTIC SUBUNIT.
                                                                                                                                         EUKARYOTA; METAZOA; EUTHERIA; RODENTIA.
  RNA-DIRECTED
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA; PRIMATES
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EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            618
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l Similarity 100.0%;
301; Conservative
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DNA POLYMERASE.
                                                                      ALLSOPP R.C.,
                                                                                                                                                                 CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2214; DB 4;
Pred. No. 0.00e+00;
0; Mismatches 0
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                                                                                                                                                                 VERTEBRATA;
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R.L., DAVIDOFF
                                                                        MORIN
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EMBL; AL022299; E1285360; -...
PFAM; PF00078; TVT.
PRNA-DIRECTED DNA POLYMERASE.
RNA-DIRECTED DNA POLYMERASE.
RNA-DIRECTED 988 AA; 116328 MW;
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NAKAMURA T.M., MORIN G.B.,
LINGNER J., HARLEY C.B., C.
SCIENCE 277:955-959(1997).
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Pred. No. 3.34e-52;
51; Mismatches 90;
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C013338; O1-JAN-1998 (TREMBLREL. 05, CREATED)
O1-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
O1-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 05, LAST SAUGUNCE UP
01-JUN-1998 (TREMBLREL. 05, LAST ANNOTATION
TELOMERASE SUBUNIT P123.
EURLOTES AEDICULATUS.
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PEAM; PEOGOT8; TVE.

RNA-DIRECTED DNA POLYMERASE.

989 AA; 116456 MW;
                                                                                                                                        SCIENCE 276:561-567(1997).
EMBL; U95964; G2072336; -.
SEQUENCE 1031 AA; 122562
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 97274210.
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LINGNER J., HARLEY C.B., CECH
SCIENCE 277.955-959(1997).
EMBL; AF015783; G2340169; -.
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                                                                                                                                                                                                                                                                                LINGNER J., HUGHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 TLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 16.9%;
Local Similarity 30.7%;
nes 65; Conservative
                                 Local
                                                                                                                                                                                                                                                   T. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-FVIRKYATIH-ATSDRATKNFVSEAFSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVLLRVVDDFLFITVNKKDAKKFLN 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDMVPFEK--VVQLLSMKT-SDTLFVDFVDYWTKSSSEIFKMLKEHLSGHIVKIGNSQYL 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTL 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLVRGVPEYGCVVNLRKTVVNFPVEDEALGGT
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   Similarity 77; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                EUPLOTIDA;
                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL EUKARYOTES;
EUPLOTIDA; EUPLOTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ES POMBE (FISSION YEAST).
ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                T.R.,
                                    9.18;
                                                                                                                                                                                                                                                                                    SHEVCHENKO A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAPMAN K.B., WEINRICH S.L., ANDREWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 375; DB 3;
Pred. No. 3.34e-52;
51; Mismatches 90
   Score
Pred.
82; M
                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDE74202 CRC32;
   Mismatches 126;
                                                                                                                                            21A885CD CRC32;
                                        201; DB 5; Length 1031;
No. 1.81e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALVEOLATA; CILIOPHORA;
                                                                                                                                                                                                                                                                                MANN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UPDATE)
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   Indels
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32;
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   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   643
   21;
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REDLINE; 97313267.

REDLINE ; 97313267.

REDLINE ; 97313267.

REDLINE ; 97313267.

REDLINE ; 1, RILES L., ALBERMANN K., ANDRE B., ANSORGE W., BENES V., BRUCKNER M., DELIUS H., DUBOIS E., DUSTERHOFT A., ENTIAN K., ROTER P., RETIAN K.D., FLOETH M., GOFFEAU A., HEBLING U., HEUMANN K., ROTER P., RA LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTL D., RA LOUIS E.J., MESSENGUY F., MEWES H.W., MIOSGA T., MOSTL D., POHL T.M., RA MULLER-AUER S., NENTWICH U., OBERMAIER B., PIRAVANDI E., POHL T.M., ROSE M., ROTRETELLE D., PURNELLE B., RECHMANN S., RIEGER M., RINKE M., ROSE M., ROSARFE M., SCHARFE M., SCHARFES M., SCHARFE M., SCHARFE M., SCHARFE M., SCHARFE M., VOLKARET G., VOSS H., WAMBUTT R., WEDLER E., VERNENDELS F., VOET M., VOLKARET G., VOSS H., WAMBUTT R., WEDLER E., VERLESCH T., WALLER F., WEDLER E., VERLESCH T., WALLER F., WEDLER E., VERLESCH T., VERLESCH 
       Matches
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q06163;
Q06163;
                                                                                                                                         SUBMITTED (JUL-1997) TO EMBL; U20618; G662136; - SEQUENCE 884 AA; 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLREL 01, 01-NOV-1996 (TREMBLREL 01, 01-AUG-1998 (TREMBLREL 07, CHROMOSOME XII COSMID 8543.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                               CHERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDLER H., ZIMMERM NATURE 387:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                  SUBMITTED
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       Local Similarity nes 68; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKLRLIPKKTTFRPI--MTF--NKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGFKFNMKKLQTSFPL 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGASVLGLDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVI-AS-II 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGFAVFNYDDVMKKYEEFVCK-WKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL
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                                                                                                                                                                                                                                        J.M.;
                                                                                                                                                                                                                                                                                                                                                                              (FEB-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIMMERMANN F.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
       Conservative
                                      6.7%;
                                                                                                                                             102662 MW;
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                                                                                                                                                                                                         EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GENBANK/DDBJ
Score 148;
Pred. No. 4.
67; Mismato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZOLLNER A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                             1A94320F CRC32;
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LLLRLVDDFLLVTPHLTHAKTFLRTLVRGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    884
                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HANI J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                  DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATA BANKS
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                                                                   Length 884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOHEISEL J.D.;
       Indels
       32;
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                805
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RESULT
AC 02
DT 01
DT 01
DT 01
OS HHGG P
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1D 051242;
AC 051242;
DT 01-JUN-1998
DT 01
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XX MEDLINE; 98065943.

XX FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,

XX FRASER C.M., CASJENS S., HUANG W.M., DODSON R., HICKEY E.K., GWINN M.,

XX LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,

XX DOUGHERTY B., TOMB J.-F., FLEISCHANN R.D., RICHARDSON D.,

XX DOUGHERTY B., TOMB J.-F., FLEISCHANN T.,

XX DOUGHERTY B., TOMB J.-F., FLEISCHANN J.,

XX DOUGHERTY B., TOMB J.-F., FLEISCHANN J.,

XX VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,

XX VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J.,

XX UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,

XX UTTERBACK T., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,

XX SMITH H.O., VENTER J.C.;

XX SMITH H.O., VENTER J.C.;

XX SMITH BOD224; -

XX EMBL; AEO01132; G2688117; -.

XX HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.9%;
Best Local Similarity 26.8%;
                                                                                      025293;
025293;
01-JAN-1998
01-JAN-1998
01-JUN-1998
GTP-BINDING
   HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI)
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; SPIROCHETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPIROCHAETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LFLSFSIIISCRVKGIVIKNGNCIKAKGISEKEILLASVSCNLHYDLNSDSINDGIKANN 71
                                                                                                                                                                                                                                                                                                                                                                                                                         LNLSKIKAFLL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILEYLRNKRPTSP-TKIYSPTQIADRI-KEFKQRLLKKFNNVLPELYFMKFDVKSCYDSI
                                                                                                                                                                                                                                                                                                                                                                     LLLRLVDDFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFDVF-LRFMCH-HAVRIRGKSYVQCQGIPQGSIL-STLLCSLCYGDMENKLFAGIRRDG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKANRDKILAVSSQSDDDTV 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVR-TVHLSNQDVIN----VV-E----M-EIF-K-T---ALWVEDKCYIREDGLFQGSSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQ-DRLTEVIASIIKPONTYCVR-RYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLNYERARRPGLLGASVLGLDDI-HRAWRTFVLRV-RA-QDPPPELYFVKVDVTGAYDTI 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVVNLRKTV-VNFPVEDEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLQETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPQGSILS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                      3 (TREMBLREL. 05, 03) (TREMBLREL. 05, 13) (TREMBLREL. 06, 15) PROTEIN (GTP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TREMBLREL. 06, CREATED)
(TREMBLREL. 06, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      936
                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 108; DB 2;
Pred. No. 6.37e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                  366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIROCHAETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637
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                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            045321
045321;
045321;
01-JUN-1998
01-JUN-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NATURE 388:539-547(1997).
NATURE 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M. DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH SONNHAMMER E., STADEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATENSTON R., WATSON A., WEINSTOCK L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., TOMB J.-F., WHITE O., KERCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITGGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLEY COTTON M.D., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                     WILKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(1994).
EMBL; Z96047; E1246680; -.
SEQUENCE 561 AA; 65807 MW; 1C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS.
OTIVABVOTA: METAZOA; ACCELOMATES; NEMATODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000571; TIGR; HP0569; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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  823
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757 PQ 758
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Local Similarity 26.4%;
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Local Similarity 25.8%;
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  ASSGLFDVF-LR
                                                    SILSSRNIFELR 94
                                                                                                   RRYAVVQKAAH-GHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVVIEQSSSLNE
                                                                                                                                                        HWNTIIRKSAHLSLYRNIFKKKRRQKLNYR-HMSTFLASSENISNIRDTVVLLEINKLSQ
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Pred. No. 2.29e-01;
25; Mismatches 25;
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Pred. No. 6.37e-02;
21; Mismatches 22
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066583; PREMBLREL 07, CR
01-AUG-1998 (TREMBLREL 07, LA
01-AUG-1998 (TREMBLREL 07, LA
01-AUG-1998 (TREMBLREL 07, LA
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Q1-FEB-1997 (TREMBLREL. 02, C
Q1-FEB-1997 (TREMBLREL. 02, L
Q1-JUN-1998 (TREMBLREL. 06, L
FLAVONOID 3',5'-HYDROXYLASE (
GENTIANA TRIFLORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AE000678; G2982926; -. SEQUENCE 1002 AA; 112414 MW; 62688CCF CPCTO.
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Q96581
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PFAM; PF00067; P450.
OXIDOREDUCTASE; MONOOXYGENASE; ELECTRON TRANSPORT; MEMBRANE;
BINDING 453
HEME (BY SIMILARITY).
SEQUENCE 516 AA; 58088 MW; F68F55B9 CRC32;
                                                                                                                                                                                                                                                                                                                                              TANAKA Y., YONEKURA K., FUKUCHI-MIZUTANI M., ASHIKARI T., KUSUMI T.; PLANT CELL PHYSIOL. 37:711-716(1996).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P4: EMBL; D85184; G1620009; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJFELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; NATURE 392:353-358(1998).
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EUKARYOTA; PLANTAE; EMBRYOBIONTA; MAGNOLIOPHYTA; MAGNOLIOPSIDA;
ASTERIDAE; GENTIANALES;
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mes 24; Conser
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26; Mismatch
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                     SUBMITTED (NOT EMBL; U17066;
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STRAIN-VACCINE STRAIN 17DD;
DOS SANTOS C.N., POST P.R.,
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VIRIDAE; SS-RNA ENVELOPED
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Best Local Similarity 32.3%;
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STRAIN-MS11;
BARTEN R., MEYER T.F.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ002783; E1198593; -.
SEQUENCE 280 AA; 31556 MW; 34FFDA18 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 15

O50469 PRELIMINARY; PRT; 280 AA.

O50469;
O1-JUN-1998 (TREMBLREL. 06, CREATED)
O1-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
O1-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
YAFJ.
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885 LLRLV 889
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2506 2506 NS5.
3410 AA; 379301 MW; 06C3D225 CRC32;
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Pred. No. 5.85e-01;
14; Mismatches 27; Indels 3;
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	; ;	Repetitis Go virus (a	Single chain polypept	Single chain binding	TRY 59	18-2-3-/TRY59.	18-2-3-/TRY202'.	18-2-3/TRY202' single	Single chain binding	Single chain polypept	Amino acid sequence o	H. pylori cell envelo	Amino acid sequence o	Amino acid sequence o	Insulin-like growth f	Amino acid sequence o	32K S2 protein encode	Sequence encoded by n	Complete WD40 peptide	Human eosinophil gran	Asurophil derived bac	Fragment of chromaffi	Agurophil-derived bac	RBE1 transcription co	Sequence encoded by c	12% S2 protein encode	Sequence of \$2-prote1	Section of the sectio	Murine interredate o.	e artio.	DBP-synthase.		pancreas G-prot	NINS-derived G	Human beta-82-crystal	ocyte activa	HB15, a member of the	protein.	rotein	intracellu	Sequence A encoded by	Type I p80 IL-1-rece	Residues 217-392 of h	Hamster islet neogene	Realdung 253-425 of 5	Turnor protests 521
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Page 3

Mon Dec 21 09:28:22 1998

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Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mean 3.259; Variance 0.721; scale 4.521

Database:

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6:part8 9:part9 10:part0 11:part11 11:part4)

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Post-processing: Minimum Match O% Disting first 1000 summaries

Searched: Scoring table:

TABLE unitprotable Gap 60

131922 seqs, 16180660 residues

Title: >US-08-951-733-14
Description: (1-949) from US08951733.pep
Perfect Score: 949
Sequence: 1 HASCORCYLLETWEALAPAT......PVEDEALGGTAFYONPARGL 949

Tabular output not generated.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Dec 10 18:50:42 1998; HasPar time 22.03 Seconds 672.605 Million cell updates/sec

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (p. 1991-198 University of Edinburgh, U.K. Copyright (p. 1991-198 University of Edinburgh, U.K. Copyright (p. 1991-198) University of Edinburgh (p. 1991-1991) U.K.

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ytokine response protein; CR3; interleukin-2; Ii-2; igand-stimulated gene expression; diagnosis; therapy; transduction.

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potassium (KIRK-3). ion channel; human

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RESULT ID WO AC WO DT 11 W08135 standard: Protein: 358 AA.
W08135 standard: Protein: 358 AA.
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The gall gene product (P70274) is known as galactose-1-phosphate
widyltransferase (transferase) the gall gene product (P70275) is
known as wridine diphosphogalactose-1-phosphatese (spinorase), and the
galk gene product (P70275) is known as galactose-1-phosphates (galactokinase). The inventors claim an TDN molecule comprising all
or part of a Streptomyces gal operon used for the expression of
coreign DNA in a transformed micro-oryanism.
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Pred. No. 3.80e+01;
0: Mismatches 0:
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. No. 3.80e+01;
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PP 11-NN-1995; DNG-1081 AS.

PR NADGETER IN.

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PP 21 - FED-1986: US-191706.

PR 20 - NAV-1981: US-191706.

PR 20 - NAV-1981: US-191706.

PR 20 - NAV-1981: US-191706.

PR 21 - OCT. 1991: US-191706.

PR 22 - OCT. 1991: US-191706.

PR 401: US-191706.

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Best Local Similarity 100.0%;
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Matches 7; Conservative
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437 LRAAVTP 443
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05-JUL-19
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Similarity 100.0%;
7; Conservative
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endoglucanase,
harzianum beta-(1,6)-endoglucanase;
) degradation; pustulanase.
harzianum.
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Pred, No. 3.80e+01;
0: Mismatches 0: In
                                         re 7; DB 17; L
1. No. 3.80e+01;
Mismatches 0
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d. No. 3.80e+01
Mismatches (
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Page 32

Gaps 0

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RESULT
ID R2
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                      Query Match 0.7%;
Best Local Similarity 100.0%;
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R26888 standard: Protein: 493
R26888: 1593 (first entry)
15-F25-1993 (first entry)
76)obs (astry acy) reductase.
761: PCB: primer.
7030da embryo.
7030da embryo.
70314816-A.
7032F7-1993.
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[[]]]]]
884 LLLRLVD 890
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|||||||
884 LLLRLVD 890
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R77163 standard: Protein: 493 AA.
R77163:
04-DEC-1995 (first entry)
05/05ba fatty acyl reductase.
Very long chain fatty acid: acyl-
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884 LLLRLVD 890
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1171111
767 AVVQKAA
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fatty-acyl-reductase.
fatty-acyl-reductase:
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fatty acyl reductase.
ong chain fatty acid: acyl-Coa;
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Pred
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Pred. No. 3.80e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Score 7; DB 14; Len
Pred. No. 3.80e+01;
0; Mismatches 0;
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d. No. 3.80e+01:
Mismatches 0:
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S5445947-A.

PM US5445947-A.

PM US5445947-A.

PM US5445947-A.

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PM US5445947-A.

PM 13-NOV-1993: 796256.

PM 10-1993: US-796358.

PM 10-1993: US-796358.

PM 10-1993: US-79636.

PM 11-1993: US-79639-A.

PM 11-1993: US-79639-A.

PM 11-1993: US-79639-A.

DN -PDDD TOAL58.

PM 12-1993-1993-A.

DN -PDDD TOAL58.

PM 12-1993-1993-A.

PM 13-1993-1993-A.

PM 13-1993-1993-A.

PM 13-1993-1993-A.

PM 13-1993-1993-A.

PM 13-1993-1993-A.

PM 13-1993-1993-A.

CC App. pspreasing the reductase CDNA was used in the construction of cape, expreasing the reductase CDNA was used in the construction of cape, expreasing the reductase In addition to a heterologous can segmentase also for wax enter prodn.

--nuence 433 AA:

O.71: Score 7, D9 14: Length 493;

'O.01: Pred No. 1804-O1: Indels
JLT 19
R6470
R76470
R76470
R76470
R76470
T 14-ALGC-1995 (first entry)
T JO-John fatty acyl-CoA reductase.
AN JO-John; fatty acyl-CoA reductase; fat
OS Simmondaia chinensia.
PH US3370996-A.
PP 23-PEB-1991 659975.
PR 23-PEB-1991 15-787351.
PR 27-SEP-1991 US-787351.
PR 27-SEP-1991 US-786256.
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PR 27-F2B-1991; US-559975.
PR 27-F2B-1991; US-569975.
PR 27-SEP-1991; US-756256.
PR 27-SEP-1991; US-776256.
PA (CALJ) LACAZEZ IC.
PA (CALJ) LACAZEZ IC.
PA (FEE 37, POLLACO NR.)
PA PSOBE 10213626 NR.)
PR NFIDE 1021362 NR.
PR NFID 
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KR 87509;

KR 87509;

CF 15-OCT-1995 ((Irst entry)

DF Resynthesised jojoba fatty-scyl-reductase.

DF Resynthesised chicensis.

NN JOSOba: fatty-scyl-reductase: ensyme: transgenic plant; wax ester:

NN JOSOba: fatty-scyl-reductase: ensyme: transgenic plant; wax ester:

NN JOSOba: Gatty-scyl-reductase: ensyme: transgenic plant; wax ester:

NN JOSOba: Gatty-scyl-reductase: plant; wax ester:

DF 01-UN1-1995; UO65116.

DF 01-UN1-1995; UO6518.

DF 01-UN1-1995;
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Best Local Similarity 100.0%;
Matches 7; Conservative
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R79934;
16-JM-1994;
10-JM-1994 (first entry)
10-J0-1994 reductase: vax-synthase: jojoba: ollseed:
Patty-acyl-reductase: vax-synthase: jojoba: ollseed:
long-chain alcohol-fatty-scyl-transferase: vax ester:
transgenic plant; crop improvement: Brassica.
sizmondeia chanesse.
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884 LLLRLVD |
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. No. 3:80e+01;
Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                   fatty acyl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n the construction of plants, e.g. oilseed a heterologous
                                                                                                                                                                                                                                                                                                   fatty alcohol.
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NOTE 10

R37485 standard: Protein: 493 AA.

R37486 standard: Protein: 493 AA.

R779110 ppp11d: cropp plant: fatty acyl: fatty alcohol acyltransfersse: 484 Acty acyl: reduced: 00050 acyl: fatty alcohol acyltransfersse: 484 Acty acyl: plantare: plantare: wax synthase: commetics: 484 Acty acyling: plantare: plantare: plantare: wax synthase: comprises nucleic acid sequence which produce wax estering: comprises nucleic acid sequence which produce wax estering wax 
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RO4869: standard: protein: 834 AA.

RO4869: protein: 834 AA.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Ps (CALT) CALEET INC.

Ps (Labaret PM. Mett JG. Pollard MR:

DR WPSDB: 075816.

PT New recombinant constructs for transforming plants of E. coli.

PT contra, nucleic acid encoding jojoba embryo long chain fatty

PT acyl-CoA reductase.

PS Claim 20: Pigure 1: JOpp: English.

CC The sequence encoding the jojoba embryo long chain fatty acyl-CoA

CC The sequence encoding the jojoba embryo long chain fatty acyl-CoA

CC The sequence encoding coli. Such constructs which in turn can be

CC used to transform E. coli. Such constructs are useful for the

CC used to transform E. coli. Such constructs are useful for the

CC used to transform E. coli. Such constructs are useful for the

CC used to transform E. coli. Such constructs

CC 1 host cells. The enzyme cattalyses the formation of a fatty

SQ Sequence 431 Ai.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Dest Local Similarity 100.0%;

Matches 7: Conservative
                                                                                                                                                        developmental stag-specific, occurring during flower stage ) to stage 2 of anther development. A method is claimed for production of male sterile plants by reducing anther specific occast settings, transgenic plants and complianted by expressing in at least the anthers of a transgenic plants occast nucleic acid, preferably is antisense of crientation. Induction of male sterility can reduce hybrid plants production costs and enables production of hybrid plants with reduced policy impossible. It also enables production of plants where this with reduced policy formation, to reduce also give reactions to such plants or to extend the life of flowers that servere upon belints or to critical plants or to reduce also give reactions to such plants or to extend the life of flowers that servere upon services of the politication, e.g. orchids. Lily CCaME (see W0018) has also been sequence 517 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 lsslrps 517
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369 LSSLRPS 375
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Pred. No. 3.80e+01;
0; Mismatches 0;
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d. No. 3.80e+01;
Mismatches 0;
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is useful for the
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JSULT 24

OR REZELIS Etandard: Protes...

C REZELIS | Ciret entry|

OT 1-OCT-1992 (first entry)

DE Varicella sonter virus polypeptide.

NY Protective: immunogenic: 99 91/coproteins: chi

NY Protective immunogenic: 99 91/coproteins: chi

NY PROTECTIVE IMPUNOGENIC: 99 91/coproteins: chi

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PT0347 standard: Protein: 854 AA.
PT0347 p301 (first entry)
PT0347 p301 (first entry)
PT0347 p301 (first entry)
PT0347 p301 (first entry)
Variceila-coster virus: (98 yene product; va
PT20313A,
PT2031A,

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2: Page 25-28: 29pp: English. The protein sequence encodes an imm which is used in the preparation of disease, varicella. The antigen is Sequence 954 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 09:28:
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884 LLLRLVD 890
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ly:peptide for use as vaccine against VZV disease and
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Best Local Similarity 100.0%:
Matches 7: Conservative
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BOSSIL 2 Standard: protein: 919 AA.

BOSSIL 2 Standard: protein: 919 AA.

10 HOUSE 1900 (first entry)

11 Displacenslypruvate carboxylase: ppc: p7011

12 Corprebacterium glutamicum.

13 E-358940-1.

14 L-559-1998 GB-02119.

14 L-559-1998 GB-02119.

15 L-559-1998 GB-02119.

16 L-559-1998 GB-02119.

17 E-559-1998 GB-02119.

18 L-559-1998 GB-02119.

19 L-559-1998 GB-02119.

10 L-559-1998 GB-02119.

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07-MAR-1996: US-012971.

(PROM) TROMESA CORP.

MULTINA A1: Seet HG:

WELL 97-202180/18.

MELL 97-202180/18.
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CY: Y chromosome: male fertility;
nor histocompatability antigen; ma
bryogenesis; spermatogenesis; tumo
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3 AKLSLQE 529
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Pred. No. 3.80e+01;
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                                                                                                                                                                                                                                                                                                                  preparate course, new bacterial DNA encoding glucosyl transferase prelates course, new bacterial DNA encoding glucosyl transferase form statisty to great higher lawers of scored carbohydrakes) in a form radialy discourse the property of the sequence represents an alpha D-glucosyltransferase from the sequence of produces soluble glucon from sucrose. A gene encoding the enzymence of the sequence and the sucrose and sucrose and produces and belong the sequence of phage lambda-cll, e.g. plassid p565501 or plassid p56501. The complex contains to be expressed in a Exchercial coll using passing possible passing possible passing possible passing possible passing possible passing possible passing p
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obd, from corporabacterium glutanicum strain odding
phesphoenolpyruvate carboxylass.
Disclosure: p. English.
ppc is important as a key ensyme in the anapierotic
and increasing oxaloacetate levels, it indirectly in
levels of L-Ma.
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Alpha-D-glucosyltransferse; primer-independent; soluble glucan
Alpha-D-glucosyltransferse; primer-independent; soluble glucan
sucrose; transgenic plant; cloning; Zenherichia coli;
phage lambd-cli; vector; plasmid po56501; plasmid po56501;
pine transfer; crop improvement; storage carbohydrate; pasture;
fendstuff; senecence; dettran; binder; food; pharmaceutical.
tersptcooccus salivarius strain ATCC 25975.
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893469 standard: peptide: 14 AA.

193469 standard: peptide: 14 AA.

193469 standard: peptide: 14 AA.

193469 standard: peptide: 14 AA.

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injurion-activator: transcription-inhibitor; plant
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Mismatches 0; Ind
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pp 01-Nov-1995; J0223B.

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(USSH) US DEI
Leonard WJ;
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wiless standard: Peptide; 12 AA.
wiless standard: Peptide; 12 AA.
wiless standard: Peptide Petide; 12 AA.
peptide Betay510 for Stat binding inhibition assay;
Probe: inhibit. Jak-Teta; signal transduction; Stat3; Stat5;
Probe: inhibit. Jak-Teta; signal transduction; Stat3; Stat5;
probe: inhibit. Jak-Teta; signal transduction; Stat3; Stat5;
inteription factor; activated; electrophoretic mobility shift;
interieukh 2 reseptor; beta chishn 1.72; RTLY-17; GAS motif;
gamma interferom activated sequence; leukaemia; proliferative disorder;
transplant rejection.
Location/Qualifiters

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co high new SHI binding spents. They represent a bissed phase library control with comprises five sendom smino cital flashing the decomputed of the stating the decomputed of the stating the decomposition assumed for the set SHI domain. These sequences were consecting the sHI domain with a mixture of peptides under conditions or permitting a ligand to bind to an SHI domain to form a complex. Any combound peptides are removed and the complexed peptides are enriched by combound peptides are removed and the complexed peptides are enriched by combound peptides are the complexes. The selected peptides are enriched by complexed the sHI domain are detected. The isolated SHI binding spentides are which bind to the SHI domain are detected. The isolated SHI binding spentides are shall be selected the conditions or diseases. Complexed SHI binding spentides are shall be specified to an SHI binding spentides are shall be specified to the selected shall be selected that shall be selected shall be selected that shall be selected shall be selected shall be selected that shall be selected sh
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an provide a structurally selective socials for interaction of functional groups. electing for interaction of functions for the production election seafoptides but with the greatly coprofiles needed for drug activity.

Query Match
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Length 15;

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APR-1998 (first entry)

Octinylated interlevkin-8 15-mer peptide ligand 15.

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Peptide;

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R61310:

R61310:

AC R61310:

Transectivating protein; Tax, peptide fragment 35.

PH HTDV: transectivating protein; Tax; regulator: host was protein protein interaction; shalbstion; virus; regulator; target molecule.

SH Human T-cell leutema Virus; regulator; taxget molecule.

FH Key Location/Qualifiers

FT modified_site 13

Inote* 'Amidated C-terminal'
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189999 standard: peptide: 16 AA.

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SULT 41

A R74374 standard: peptide: A...

B R74374 standard: peptide: A...

C R7437, 1996 (fire entry)

OF HTLVAN-1996 (fire entry)

OF HTLVAN-1996 (fire entry)

OF HTLVAN-1996 (fire entry)

Not HTLV-1 peptide: TAX20: residues 286-308; adult T-cell leub

Not HTLV-1 associated myslopath;

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Not US$430244-A.

PD 10-MAY-1995: 103742.

PR 06-AGC-1993: 103742.

PR (US$43-01-1993: 103742.

PR (US$41-01-1993: 103742.
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/notes *Amidated C-
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Of 37-NOV-1995 (first entry)

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DE .cetarrhalis (D epicope containing oligopeptide.)

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NW CD protein Branhamelia.

PR 20-828-1994; U1993;

PR 20-828-1994; U1993; U1994; U1994; U1994;

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Example 1: Columns 11-12: 21pp; English

Example 1: Columns 11-12: 11pp; English

17(1356-74)75 are himsan T-cell lymphotropic virus type I (HTLV-I)

17(1356-74)75 are himsan T-cell lymphotropic virus type I (HTLV-I)

17(1356-74)75 are himsan T-cell lenkaemia, and HTLV-I, e.g. adult T-cell lenkaemia, and HTLV-I, sequence 20 AA;
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Tax protein fragment, HTLV-1, human T-cell leukaemia vitus; hepatitis B;
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human lymphotepia vitus, tenn-settveting factor inhibitor; therapy;
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homosypous familial hypercholesterolaemia; cancer.
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targetting polypeptide; suppression; immune responses; transplant rejection.

Transplant rejection.
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Wijill Standard: peptide: 25 AA.

Wijill Standard: peptide: protein: inhibitor: transmembrane domain: RM Antagonist: integral membrane protein: inhibitor: disease: Parkinson's disease: RM peptide ulcer; glaucoma: asthma: renal disease: Autoimmune disease: RM peptide ulcer; glaucoma: asthma: renal disease: Autoimmune disease: RM peptide ulcer; glaucoma: asthma: renal disease: Autoimmune disease: RM peptide ulcer; glaucoma: asthma: renal disease: Autoimmune disease: RM peptide ulcer; glaucoma: asthma: renal disease: Autoimmune disease: RM peptide ulcer; glaucoma: asthma: renal disease: Autoimmune disease: RM peptide ulcer; glaucoma: Autoimmune disease: Pattinson: glaucoma:
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Of C-protein coupled codorant receptor I7 N-terminal sequence.

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Nismatches 0;
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WESTERNAMENT HE ANNAL SERVICES.

PH (1958H) 195 US-94812 HONAN SERVICES.

PH (1958H) 195 US-94812 HON
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(H1232) standard; peptide: 28 AA.

(H1232) standard; provin (releasing hormone analogue; release;

(H1232) standard; provin (releasing hormone analogue; release;

(H1232) standard; provin (releasing hormone analogue; release;

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(H1232) standard; peptide: 28 A.

(H1232) standard; peptide: 28 AA.

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Best Local Similarity 54.5%;
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PR 14-APR-1996; UM-582.

PR 14-APR-1996; UM-582.

PR 16-APR-1996; UM-582.

PR 16-APR-1
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18. 11.00 Alaboxy Comentary

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X= 1-6C alkyl, 1-6C hydroxyalkyl,
1-6C acyl, 2-6C hydroxyacyl",
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                            US-08-951-733-14.
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RESULT 49

Refs02 standard: Peptide: 35 A..

No w46502 to the Alpha-glucuronidase protein.

DT 18-WAT-1998 (first entry)

DE Peptide 2 of the Alpha-glucuronidase protein.

RW Alpha-glucuronidase: Aspecgillus tubigensis W7756: overexpression) tres

RW degradation: plant matter: animal feed: metal ion; blosvallability.

RW degradation: plant matter: animal feed: metal ion; blosvallability.

RW feelillus tubigensis.

PH Rey clifference 1 Coathon/Qualifiers

FT Mise_difference 2 /note= "represents any amino acid"

"" "mino_difference 2 fote= "represents any amino acid" Ouery Match 0.6%; Best Local Similarity 100.0%; Matches 6; Conservative can be used to treatment of Ho the DNAs can be mammal against Sequence 32; 6 ggsasr 11 ||||||| 247 GGSASR 252 to develop products for the (
f HCV infection. The peptide
n be used in the preparation onst HCV infection.

32 AA; Pred. re 6; DB 23; Leng d. No. 4.71e+02; Mismarches 0; diagnosis, prevention and sequences and vectors containing of a vaccine to immunise a Length 32 ő Cape

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RESULT 50

ID W20450 standard: Protein: 45 AA.

RO W20450 pp. (first entry)
DE H. Polori secreted or periplasmic protein, 3544551 as.

RO W20450 pp. (first entry)
DE H. Polori secreted or periplasmic protein, 3544551 as.

RW Hoppiasmic vaccine: Prevention: breament: infection: activator: RW Hoppiasmic vaccine: Provention: breament: infection: activator: RW Hoppiasmic vaccine: Provention: RW Hoppiasmic vaccine: Provention: RW Hoppiasmic vaccine: Proventiasmic protein: RW Hoppiasmic vaccine: RW Hoppiasmic vaccine: Proventiasmic protein: RW Hoppiasmic vaccine: RW Hoppias
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Search completed: Fri Dec 18 18:54:12 Job time: 210 Secs.
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                                                                                                      8 alfevi 13
||||||
682 ALFSVL 687
                                                                                                                                                                                                                                                                                                                acid sequences predicted from various OFF were analysed for significant homology to other known or exported membrane protesins. Reving identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production. e.g. in E. coll hosts.
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300 6 0.6 386 3 50899) 301 aignal sequence recept 138+02 302 6 0.6 288 2 506030 gentamicin y-to-cety 138+02 303 6 0.6 288 2 506030 gentamicin y-to-cety 138+02 304 6 0.6 288 2 506030 gentamicin y-to-cety 138+02 305 6 0.6 289 2 105506 water sincel y-to-cety 138+02 305 6 0.6 289 2 105506 water sincel y-to-cety 138+02 305 2 105506 water sincel y-to-cety 138+02 307 2 50775 water since y-to-cety 138+02 308 2 105506 water sincel y-to-cety 138+02 309 2 105506 water sincel y-to-cety 138+02 300 2 50775 water sincel y-to-cety 138+02 301 2 50775 water sincel y-to-cety 138+02 302 2 50775 water sincel y-to-cety 138+02 303 2 50775 water sincel y-to-cety 138+02 304 6 0.6 303 2 50503 water sincel y-to-cety 138+02 305 6 0.6 303 2 50503 water sincel y-to-cety 138+02 305 6 0.6 303 2 50503 water sincel y-to-cety 138+02 307 2 50503 water sincel y-to-cety 138+02 308 2 50503 water sincel y-to-cety 138+02 309 2 50503 water sincel y-to-cety 138+02 300 2 50503 wat	Man Dec 21 09:28:23 1998 U9-08-951-733-14-rpr	Carlin efflux system Oct. 5022 1 J05556 Oct. 5022 1 J05557 Oct. 5022 1 J05557 Oct. 5022 1 J05557 Oct. 5022 1 J05577 Oct.	Mon Dec 21 09:28:23 1999 US-08-951-733-14.xpr
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	116 0.6 877 2 85168) dnaK-type melecular c	Mon Dec 21 09:28:23 1988 US-08-951-733-14.rpr	### STATE OF THE PROPERTY OF T	Mon Dec 21 09:28:23 1998 US-08-951-733-14-xpr
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	Page 20	•	Page 18

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	Page 23	
**coession A(0); leukocyte common antigens. **colous type prottin **colous type man **co	Mon Dec 21 09:28:23 1998 US-08-951-733-14.rpr	CENTICS CLASSIFICATION Superimity leukocyte common antigen; leukocyte common profest rytosine phosphates bomby; profess programs profess rytosine phosphates bomby; profess

Page 24

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Page 22

\$87-1291 64,150,161,207,211, 218,251,258,290, 311,322,347,416, 427,457,489,520, 81 24-564
24-30,170-1291 esanus predicted slabsh MAT,
sproduct protein-tyrosine-phosphatase (T-cell variant)
escatus predicted slabsh MAT,
domain transmembrane seatus predicted slabsh TAN,
domain transmembrane seatus predicted slabsh TAN,
domain transmembrane satus predicted slabsh TAN,
domain intracellular satutus predicted slabsh INTN,
domain intracellular satutus predicted slabsh INTN

Oeery Match 0.9%; Score 9; DB 2; Length 1191; Best Local Similarity 100 0%; Pred, No. 974e-04; Matches 9; Conservative 0; Mismatches 0; Indels 0;

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te Cys (phosphocysteine intermediate) *status

ACCESSIONS REFERENCE *authors *journal *title ORGANISM DATE RESULT ENTRY TITLE Db 8 LAPGFALLD 16 ||||||||| Oy 119 LAFGFALLD 127 A23652 etype fragments
protein kinase (CC 27.1.137), cAMP-dependent, type II-alpha
regulatory chain - pig (fragments)
formal_name sub-servis domestics (common_name domestic pig
10.ynn_1988 sequence_revision 05-Mar-1993 stext_change

Hemmings, B.A.: Schwarz, H.: Adavani, S.R.: Jans, D.A. (** PEBS Lett. (1986) 209:119-222

Expression coloning of a count encoding the type II regulatory aubunit of the CMP-dependent protein kinase.

ces MUID: 87080763

Potter, R.L.: Taylor, S.S.
J. Biol. Chem. (1979) 234.9000-9005
Correlation of the AAN binding domain with a site of autophosphorylation on the regulatory subunit of

Mon Dec 21 09:28:23 1998

ACCESSIONS REFERENCE Sauthors Sjournal Stitle ENTRY
TITLE
ORGANISH
DATE

Score 8: DB 1: Length 305: Pred. No. 1.29e-01: 0: Mismatches 0: Indels 0: Capa

0

TYRYN9 stype complete

protein finase (EC 2.71.37) MOS (clone twis) .

myeloproliferative sarcoma virus

ALTERNATE_NAMES kinase related transforming protein MOS; MOS proto-oncogene

ORGANISH cformal_name myeloproliferative sarcoma virus

60rmal_name myeloproliferative sarcoma virus

10-me-1988 sequence_revision 11-Dec-1988 stext_change

20-Mar-1998

ACCESSIONS ASSECT

Tiel. J.: Stocking. C.: Stacey, A.: Ostertag, W.

"Virol. (1987) 55:889-87

remperature-sensitive mutant of the mysloproliferative
sacrosa virus, altered by a point mutation in the mos
acrosa virus been modified as a selectable retroviral
oncogens, has been modified as a selectable retroviral

ACCESSIONS REFERENCE Sauthors Sjournal Stitle

US-08-951-733-14.zpr

DGBES9 "type complete 13.2.2.") - human herpesvirus 3 uracil DNA 9jocas/lase (Ed 3.2.2.") - human herpesvirus 3 tormal_name human herpesvirus 3, varicella-coster virus 30-Sep-1888 stext_change 114.Nov-1897

*Authors Davison, A.J.: Scott, J.E.

*Journal J. Gen: Virol. (1986) 67:2759-1816

*Itile
erosareference**MUID:86306857

**accession G27215

**smolecule_type_DNA

fresiduce

erosareference**EMBL:XX4170: NID:959989; PID:960048

#gene 59
CLASSIFICATION #superfamily uracil-DNA glycosylase
RIPMORDS 91ycosidase: hydrolase
SUMMARY #length 305 #mblecular-veight 34376 #checksum

Query Match 0.8%; Best Local Similarity 100.0%; Matches 8; Conservative

ecross-references MUID:87113002
eaccession A36592
esmolecule_type DNA
earesidues 1-342 estabel DNA 1-342 estabel FRI

> ă Dec 21 09:28:23 1998

Page 27

US-08-951-733-14.

SECTIONS - references GB:M15424: NID:g3327210: PID:g3327211
GENETICS
GENETI

FEATURE 61-341 69-77 90 SUMMARY KEYWORDS #domain protein kinase homology #label KIN\
#region protein kinase ATP-binding motif\
#active_site Lys #sactus predicted
#length 342 #molecular-weight 37970 #checksum 8888 mos
superfamily kinase-related transforming protein: protein
kinase homology
ATP: oncogene; phosphotransferase; serine/threonine-specific
protein kinase; transforming protein

Query Match 0.8%; Score 8; DB 1; Length 342; Best Local Similarity 100.0%; Pred. No. 1.26-01; Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps

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Db 291 LRPSLTGA 298 |||||||| Cy 372 LRPSLTGA 379

ACCESSIONS REFERENCE Fauthors Fjournal Stitle ORGANISM DATE RESULT ENTRY TITLE OKBOAR **type complete
protein kinase (CC 27.1.137), cAMP-dependent, type II-alpha
regulacy ohain bowine
*formal_name dos prinigenine kaurus *common_name cattle
formal_name dos prinigenine kaurus *common_name cattle
formal_name dos prinigenine kaurus *common_name
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19-bay-1992*

kio, K.: Smith, S.B.: Krebs, E.G.: Walsh, K.A.: Titani, K. cochemiatry (1984) 33:4200-4205 to the content of bovine type into acid sequence of the regulatory subunit of bovine type II adenosine cyclic 3',5' phosphate dependent protein

ecross-references MDID:91378531
saccession e17059
stroblocule_type protein
streatione = 155-156 stabbl BBA
extractione = 155-156 stabbl BBA
extractione = 155-156 stabbl BBA

Page 25

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11740 (1980) 255.8439.4488

O. Biol. chem. (1980) 255.84839.4488

O. Biol. modification of an adenosine 3':5'-monophosphate binding site of the regulatory subunit of cNP-dependent protein kinase II with 8-axidoadenosine 15'-monophosphate.

115'-monophosphate.

A15740

*across:references MUID:81000004
*accession A13740
*secession A13740
*secession A13740
*secession 136-189 salabel MER
*residues 136-189 salabel MER
*composed of two regulatory
chains and two catalytic chains. Activation by call produces two
chains and two catalytic monomers and a resultatory distribute binds four
active catalytic monomers and a resultatory distribute binds
*composition**
Composition
**Compo

COMMENT COMMENT COMMENT o NMP molecules

Four types of regulatory chains are found: I sliphs, I bets, if shiphs, and II bets, their expression varies among tissues and is in some cases constitutive and in others inducible. Type II regulatory chains are phosphorylated by the attivated catalytic chain. The physiological significance of phosphorylations by other kineses is unclear catalogic by a completing proteins including chains are acceptable as a constitution of the phosphorylations of the mediate seminants association by binding to anothering proteins including chains accept the phosphorylations of the seminant special control of the binding and for district extraction.

CLASSIFICATION superfamily cAMP-dependent protein kinase regulatory chain: cAMP receptor protein cyclic nucleotide binding domain

FEATURE 81·155 KEYWORDS #domain cAMP receptor protein cyclic nucleotide-binding domain homology (fregment) #label CAP #length 169 #checkeum 765 cAMP binding: duplication: heterotetramer; homodimer; phosphoprotein; phosphotransferase

SUMMARY Opery Match | 0.8%; Score 8; DB 2; Langth 169; Best Local Similarity 100.0%; Pred No. 1.29e-01; Matches 8; Conservative 0; Mismatches 0; Indels 0; Caps

RESULT 5 52 EEEDTOPR 59 ||||||||| |61 EEEDTOPR 468

Page 28

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chains and two catalytic chains. Activation by cANP produces two active catalytic monomers and a regulatory dimer that blands four CANP molecules.

The production of the catalytic monomers and a regulatory dimer that blands four the production of the catalytic chain. Their expression varies among tissues and in others inducible. Their exputatory chains are phosphorylated by the activated catalytic chain. The physiological significance of phosphorylations by other kinases is unclear. The physiology chains mediate membrane association by binding to anchoring proteins. Including the parts kinase. The

COMMENT

COMMENT CLASSIFICATION preson the control of perfamily cAMP-dependent protein kinase regulatory chain:

Keywords

red amino end; cAMP binding; duplication; retramer; homodimer; phosphoprotein;

204,213 334,343 SUHMARY FEATURE 1-134 135-256 48.211 95 257-389 *domain protein interaction *label DIN\
*domain borotein interaction *label DIN\
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*modified_afte activated maino end (Ser) *status
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proline-directed kinase) *status predicted\
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autophosphory/arion) *status experimental\
*binding_aite cAMP (Cli, ANY) *status predicted\
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Query Match 0.8%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 400; Pred. No. 1.29e-01; 0; Mismatches 0; Indels 0; Gaps 0

OKHUJR stype complete
protein kinase (CC 27.1.17), cAMP-dependent, type II-alpha
regulatory chain - human
formal_name homo sapiens ecommon_name man
thail_name lomo sapiens ecommon_name man
1.Har-1993 secquence_revision 31.Har-1993 stext_change
02-Sep-1997

Mon Dec 21 09:28:23 1998

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O.09; Score 8; DB 1; Length 404; Best [Coal Similarity 100.09; Pred No. 1, 29-01; Maches 9; Conservative 0; Mismatches 0; Indels 0; Gaps elength 404 emolecular-weight 45518 echecksum 9820

Db 110 EEEDTDPR 117 [[1]||||| Qy 461 EEEDTDPR 468

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ORGANISM DATE

ACCESSIONS
REFERENCE
*authors
*journal
*title

Nomura, O.: Nakabayashi, O.: Rishimori, R.; Misuno, S. Gene (1977) 185:117-212
The CDNA cloning and transient expression of a chicken gene encoding cytochrome P-450scc.
Adrenal gland
126200

CLASSIFICATION
RETWORDS
FEATURE
452 realectic type mRM. | 1508 #1.4bel NOM | | 1508 #1.508 #1.4bel NOM | 1508 #1.508 #1.508 | 1508 #1.50

poscol
superfamily cytochrome P450
heme: steroid binding

SUMMARY sbinding_site heme iron (Cys) (axial ligand) estatus predicted elength 508 emplecular-weight 58195 echecksum 7347

Ouery Match 0.8%; Score 8: DB 2: Length 508; Best Local Similarity 100 0%; Pred No. 1380-01; Ddels 0; Matches 8: Conservative 0: Mismatches 0; Indels 0;

0

Db 128 PYGVLLKT 135 |||||||| Qy 426 PYGVLLKT 433

10

ALTERNATE_NAMES

HHBYS1 stype complete
dnaK-type molecular chaperone SSC1 precursor, mitochondrial
yeast (Saccharconyces cerevisiae)
endonuclease SceI 75K chain: endonuclease SceI large chain:

Mon Dec 21 09:28:23 1998

Page 31

US-08-951-733-14.zpr

heat shock protein 70-related protein SSC1; protein GTF654; protein J1639; protein KJR046; Gormal_name saccharomyces crevisiae 7-Jun-1992 sequence_revision 30-Jun-1993 *text_change

**authors Craig, E.A.: Kramer, J.: Shilling, J.: Werner-Washburne, M.:

**sjournal Mol. Cell. 1861, (1989) \$1000-7006

**title Scil, on essenttal member of the yeast HSP70 multigene

**cross-references MUID: 89384560

**accession A3489

**snolecule_type DNA

**sreaidues 1654 **slabel CRA

**sreaidues 1655 **slabel CRA

**sreaidues 1655 **slabel CRA

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withing, N.; Hakzers, K.; Yammoto, E.; Shibata, T.
J. Blol. Chem. (1990) 265:15199:1197.

a subunit of year site-specific endonuclease Scalis a
mitocohondrial manual control of the 70-kDa heat shock protein.

stury 190169701

S11176

scross-references NUID:91092234

**Recession 512497

**Recession 512497

**Testion 127610

**Testion 1

FERENCE \$57052 (A. J. Tanava, DARE Sauthors Hunny M.E.; Chust, J.C.; Galibert, F. sauthors audmitted to the Protein Sequence Database, saccession \$57064 molecule type DNA Temidues - 1-654 felabel MAN Temidues - 1-654 felabel MAN TEMEGETERIES EMBL: 248945; NID:91015700; PID:91015701; NIPS:YJR045c TEMEGETERIES EMBL: 248945; NID:91015700; PID:91015701; NIPS:YJR045c

Huang, M.E.; Chuat, J.C.; Galibert, F. Yeast (1995) 11:775-781

Mon Dec 21 09:28:23 1998

ACCESSIONS REFERENCE Pauthors

Page 29

Page 30

US-08-951-733-14. rpr

SO3885 SO3885 Oryen, O.; MyXlebust, F.; Scott, J.D.; Hansson, V.; Jahnsen,

#journal PERS LET. (1983) 246-57-64

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OABY-dependent protein kinase encodes an alternate
animo-terminent protein kinase encodes an alternate
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Tobaina and two extalvide Obaina Activation by CAMP produces two

estive catalvide Obaina are jound: I-alpha. I-bata.

COMMENT Proper Of regulatory chains are found: I-alpha. I-bata.

II-alpha and II-bata. Their extression varies among tissues and

II-alpha, and II-bata. Their extression varies among tissues and

II-alpha, and II-bata. Their extression varies among tissues and

II-alpha, and II-bata. Their extression varies among tissues and

II-alpha, and II-bata. Their extression varies among tissues and

ia-ia name cases constitutive and in others inducible.

COMMENT Type II regulatory chains are plosphorylated by the activated

condent Type II regulatory chains mediate membrane association by binding

to anothering processor, including the AMP tissue. The

amino terminal 50 residues are essential for this binding and for

dimeritarion.

#gene
#Geros.references.CDB.120314; ONIN:176910
#map_position 7pter-7p22
CLASSIFICATION #syperfamily CAMP-dependent prot KEYWORDS *superfamily cAMP-dependent protein kinase regulatory chain: cAMP receptor protein cyclic nucleotide-binding domain

etylated amino end: cAMP binding; duplication; heterotetramer; homodimer; phosphoprotein; phosphotransferase

FEATURE 2-404 2-138 139-260

product pocean kinase, cAMP-dependent, type II-alpha regulatory calls setate predicted slabel HAT domain protein interaction #label DIM sedomain chap receptor protein cyclic nucleotide-binding domain chap receptor protein chap sedomain chap receptor protein chap sedomain chap receptor in chapter domain chap receptor in chapter domain chapter compared the compared co

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binding_site phosphate (Ser) (covalent) (by autophosphorylation) satatus predicted\ binding_site cAMP (Glu, Arg) satatus predicted\ binding_site cAMP (Glu, Arg) satatus predicted

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Analysis of a 42.5 kb DNA sequence of chromosome X reveals three CRNA genes and 14 new open reading frames including a gene most probably belonging to the family of ubiquitin-protein ligases. US-08-951-733-14.rpr

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highly homologous to inositol polyphosphata-5-phosphatase.

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serosa-references GD:S0001445; MTP5:YTR006c

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                                                          ssatatus nucleic acid sequence not shown semblecule_type_DNA seresidues 36-355;640-688 salabel VOW secross-references_EMBL:X79743
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Nucleocide sequence and analysis of the centromeric review 550-98 chromosome IX.
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Blochem, Biophys. Res. Commun. (1991) 18:1111-1136
Blochem, Biophys. Res. Commun. (1991) 18:1111-1136
Insulin-like growth factor-binding proteins in porcine
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insuiln-like growth factor binding protein 2 - pig (fragment) 
formal_name Sus scrofa domestica 4common_name domestic pig 
11-Mar-1997 aquence_revision 31-Mar-1992 *text_change 
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Shimasaki, S.: Gao. L.: Shimonaka, M.: Ling, N. Nol. Endocrinol. (1991) 5:938-948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *authors Shimada, R.: Whittier, R.F.: Hiratsuka, J.; Maeda, Y.: Hirai,
*submission submitted to JIPID, December 1989
*accession 000382
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                   901945 stype fragment myosin catalytic light chain, ventricular and slow striated
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REFERENCE SUBJECT SOLIPS SUBSTRAINT PROBLEM S. SOLIPS S. Buckingham, H.B.

sjournal Nucleic Acids Res. (1989) 16:10037-10052

rittle Promoter analysis of myosin sikali light chain genes expressed in mouse attiated muscle.

scross-references My10:89057447

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thyroturphn receptor - guinea pig (fragment)
fformal_name_cavia_porcellus foommon_name guinea pig
19-Dec_1991 #sequence_revision 18-Nov-1994 #teatt_change
06-Jun-1997 Roselli-Rehtuss, L.; Robbins, L.S.; Cone, R.D.
Endocrinology (1922) 101:187-1861
Diyrotropin receptor messenger ribonucleic acid is expressed
in near brown and white adipose tissues in the guines pigrose, MCID: 9239.88 0

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Submission submitted to the EMSL Data Library, April 1991 **Redescription Nucleotide sequence of Mansenula polymorpha DNA region sections of S14855 *Submission Submission S

614855 \$14854 \$14854 Krittlina, A.I.; Seregina, S.A.; Tikhomirova, L.P.; Kryukov,

\$14855 etype complete
htypothetical protein 7 - yeast (Hansenula polymorpha)
formal_name Hansenula polymorpha
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46 LKELVAR 52 ||||||| 99 LKELVAR 105

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Page 38

RESULT 18
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X33329 erype fregment Ky-5:0 glycoprotein mouse (fregment) fformal_mane Nus musculus *common_name house mouse 65-Jun_1087 sequence_revision 05-Jun-1987 etext_change 20-Mar-1998

ACCESSIONS REFERENCE Pauthors

*journal

Shen, F.W.; Saga, Y.; Litman, G.; Freeman, G.; Tung, J.S.; Cantor, H.; Boyee, E. Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7360-7363

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***CLASSIPICATION ***Superfamily leukocyte common antigen: leukocyte common antigen: cytosite; domain bomology;

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hypothetical protein - Symechocystis sp. (PCC 6801) stormL_name Symechocystis sp. pcc 6801 sp. 15-pgr 1997 sea----
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Amaura, Y.; Hiyajina, N.; Hirosawa, H.; Sugiura, N.;
Amorto, S.; Kimura, T.; Hosauchi, T.; Matanno, A.;
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Immunogenetic [1986] 24:17-23
The complete primary structure of the T-cell receptor genes
from an alloreactive cytotoxic human T-lymphocyte clone.
The complete primary structure of the property of the complete primary structure.
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Mon Dec 21 09:28:23 1998
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697 LLGASVL 703
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GENETI ACCESSIONS REFERENCE SAUCHORS Sjournal Stitle ORGANISM DATE O.7%; Score 7; DB 2; Length 148; Best Local Similarity 100.0%; Pred. No. 1.04e-01; Best Local Similarity 100.0%; Pred. No. 1.04e-01; Indels 0; Gaps Matches 7; Conservative 0; Mismanches 0; Indels 0; Gaps hbcR DNA binding: transcription regulation elength 149 smolecular-weight 17255 schecksum 5904 SIO280 *type complete

#Cormal_name Eacherichia coli

#Cormal_name Eacherichia coli

10-Sep-1993 **equence_revision 10-Sep-1993 *text_change

09-Sep-1997 IT; D.I.: Fawcett, T.: Cooper, R.A.
Gen Genet (1991) 2017-201-250
Each Therichia coli C homoprotocatechuate degradative
peron: hpc gene order, direction of transcription and
on crol of expression. 9

SECULIA SERIOS ENTRE COMPLETE

ITTLE hypothetical protein FLL042c - yeast (Saccharomyces

FLTRE hypothetical protein L0737

ORGANISH COTTAL Jame Saccharomyces cerevisiae

OL-May-1995 - sequence_revision 14-May-1996 ftext_change

14-Nov-1997 esidues 1:167 salabel MZD ross-references EMBL:273147; NID:gl160216; PID:e245470; PID:gl160137; ross-references EMBL:273147; NID:gl160216; PID:e245470; PID:gl160137; Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R. submitted to the Protein Sequence Database, May 1996 564794

Mon Dec 21 09:28:23 1998 697 LLGASVL 703 US-08-951-733-14.rpr

RESULT 24 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE Pauthors Pjournal stitle Hishida, T. Iwasaki, H.; Ishioka, K.; Shinagawa, H. Gane (1986) 182:63-70
Noiseullar analysis of the Pseudomonas seruginosa genes, ruwh, ruw and ruwc; involved in processing of homologous recombination intermediates. CS478 type complete - Pacudomonas aeruginosa ndodeoxyribonuclease ruvc - Pacudomonas aeruginosa formal_name Facudomonas aeruginosa seruginosa - 7-3uli-1997 aequence_revision 39-Aug-1997 atext_change - 28-Sep-1997

GENETICS sgene FEATURE 2-174 Raccesion UC5478

**Remolecule_Type_DNA

**remiduces_remole_108136; MID:gl183837, PID:dl012484; PID:gl183840

**Cross-references_DDBJ:D83136; MID:gl183837, PID:dl012484; PID:gl183840

**Experimental_Source_strain_PAOl

SUMMARY **product endodeoxyribonuclease ruvC **status predicted **abbel MAT endodeoxyribonuclease ruvC **status predicted **Length 174 **smlecular-veight 19556 **chacksum 8754 Length 174;

Db 164 GARRRGG 170 11111111 Qy 242 GARRRGG 248 O.7s. Score 7; DB 2; Length 174; Best Local Similarity 100:09; Pred. No. 1 (Ode+0); Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

RESULT 25 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE FAUCHOIS \$1,240 "type complete
yop20 protein 'Terainia enterocolitica
formal_name 'terainia enterocolitica
cormal_name 'terainia enterocolitica
10-mov-1995 *text_change
09-Sep-1997 Cichela, T.; Mattiau, P.; Brasseur, R.; Ruysschaert, J.M.; Cornelis, G. erfect, Imaun. (1990) 58:240-2849 er MOID:9035044

Mon Dec 21 09:28:23 1998

Page 43

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\$14240

GENETICS #accession 51420 #accession preliminary #molecule_type DNA #residues 1-182 #slabel NIC:948602; PID:948604 ##Cross-references EMSL:X52733; NID:948602; PID:948604

O.7%; Score 7; DB 2; Langth 182;
Best Loat Similarity 100 0%; Pred No. 104e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps yop20 elength 182 emolecular-veight 20828 echecksum 1492

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Db 62 GSILSTL 68 . |||||||| Qy 856 GSILSTL 862

EXPRY MORTLY stype complete

TITLE myosin shail light chain 3, ventricular and slow skeletal

ALTERNATE, NAMES MICHAEL KICA'N: myosin Li catalytic light chain, cardiac

REALER MICHAEL MICHAEL MORTLY CHAIN 1

FOR 1891 sequence_revision 03 oct-1995 stext_change

OKLER 12-Feb-1993 sequence_revision 03 oct-1995 stext_change

OKLER -1997 Sequence_revision 03 oct-1995 stext_change RESULT 26 ENTRY TITLE

ACCESSIONS REFERENCE eauthors ejournal stitle KERAILY, E.M.: Buttrick, P.M.: Leinwand, L.A.
Nucleic Acids mes. (1889).12755-2765
venticular myosin 19ht chain 1 is developmentally regulated
venticular myosin 19ht chain 1 is developmentally regulated
venticular myosin in hypertension.
cos MUID:89340011

; \$15759; \$06169

*crossion 609573
*molecule_ype mRNA
*molecule_ype mRNA
*srcadues 1 - 200 *slabel MCN
*srcadues 2 etitle Periasany, M.; Wadgaonkar, R.; Kumar, G.; Martin, B.J.; Siddiqui, M.A.O. Nullic Acids Res. (1988) 17:7733-7734 Characterisation of a rat myosin alkali light chain gene expressed in ventricular and slow twitch skeletal muscles. 515759

*Accession \$15759

**Recission \$15759

**Recission \$15759

**Cross **Cerence BEGL: X15315; NID: 956671; PID: 9763179

**Cross **Cerence BEGL: X15315; NID: 956671; PID: 9763179

**Introne 40/1; 50/1; 100/1; 166/1; 192/1

Mon Dec 21 09:28:23 1998

Page 41

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Page 42

stexperimental source strain S288C GENETICS

*Bmap_position 12L SUMMARY slength 167 *molecular-veight 19759 *checksum 3500

O.7%; Score 7; DB 2: Length 167;
Best Local Similarity 100:06; Pred No. 1.04e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 36 DGLLLRL 42 |||||||| Qy 882 DGLLLRL 888

ORGANISM DATE RESULT 23 ENTRY TITLE 504916 "type fragment
T-cell receptor delta chain recursor V-D-J region (clone
KT08A) - human (fragment)
Fframil_nem knoment socmmon_name man
10-5ep-1991 sequence_revision 30-5ep-1991 *text_change
08-5ep-1995 pt.0078

ACCESSIONS REFERENCE sauthors *title Takihar, Y.; Reimann, J.; Hichalopoulos, E.; Ciccone, E.;
MOTETLA, L.; Mak, T. M.;
J. Exp. Med. (1989) 169:393-405
Diversity and Structure of human T cell receptor delta chain
genes in peripheral blood gamma/delta-bearing T
juppbocytes
noces MJD:89094239

eaccession 504

CLASSIFICATION RETWORDS FEATURE 1-26 27-168 tion 804916
licule_type_mRW,
licule_type_mRW,
oss-reference_BDEL_X14548; NID:g37299; PID:g37300
reference_BDEL_X14548; NID:g37299; PID:g37300
reference_tomaily_immunogiobulin v region; immunogiobulin homology
TTON regin receptor

Admain signal sequence *attau** predicted ***label SIC\
***product T-cell receptor data chain (fragment) ***attau*
**predicted *!habel Walla-5 | slabel Walla-6 |
**Admain V region (J-data-1) **!abel JEC\
**Admain (J-data-1) **!abel JEC\
**Admain (J-data-1) **!abel CRE
Jength 160 *Checksum 1221

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative 4 LLGASVL 10 Score 7; DB 2: Length 168; Pred. No. 1.04e+01; 0; Hismatches 0; Indels 0; Gaps

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FEATURE 54-88 133-165 168-200 RESULT 27
ENTRY
TITLE
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DATE Db 30 AAPEPER 36 ||||||| Qy 264 AAPEPER 270 SUMMARY CLASSIFICATION KEYWORDS O-TY Score 7: DB 1: Length 300;

Best Local Similarity 100.0%; Pred. No. 104e+01;

Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps #domain calmodulin repeat homology #label EF1\
#domain calmodulin repeat homology #label EF1\
#domain calmodulin repeat homology #label EF1\
#domain calmodulin repeat homology #label EF1\
#modified_mite blocked amino end (Pro) (in mature form)
#fattus predicted
#length 200 #molecular-veight 22156 #checksum 3898 G89784 "type complete hypothetials subtilis hypothetials protein ydMt. Bacillus subtilis former.lps7 sequence_revision 05-Dec-1997 stext_change 05-Dec-1997 sequence_revision 05-Dec-1997 stext_change 05-Dec-1997 superfamily calmodulin; calmodulin repeat homology blocked amino end; calcium binding; cardiac muscle; duplication; EF hand; muscle contraction; skeletal muscle F.: Ogasavara, N.: Moszer, Hellado, R.P.: Misuno, M.: Noone, D.: O'Reilly, B.: Park, S.H.: Parro, tillet, S: Brans, treer, M. H. Landings, M.J. Landi

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RESULT 28
ENTRY
TITLE
CONTAINS
ORGANISM

WAAD87 stype complete
early ELA 28K protein - Numan adenovirus 7
early ELA 24K protein
stormal_name Mastadenovirus h7 scommon_name human adenovirus

host Homo sapiens (man) 18-Dec-1981 sequence_revision 18-Dec-1981 stext_change 16-Feb-1997

Db 105 VTGAYDT 111
0y 735 VTGAYDT 741

O.7%; Score 7, DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.04e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

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ydhK slength 205 *molecular-weight 22536 *checksum 3012

Nature (1997) 390:24 The complete genome Bacillus subtilis.

ne sequence of the Gram-positive bacterium

preliminary; nucleic acid sequence not shown: translation not shown

Onote DATE

ACCESSIONS REFERENCE *authors

RESULT 29 SUMMARY FEATURE 1-163, 195-261 ouery Match 0.7%; Score 7; DB 1; Length 261;
Best Local Similarity 100.0%; Pred No. 1 04e+01;
Macches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 1-261 selabel DIJ
superdamily adenovirus early ElA protein
elternative spilcing; DNA binding; early protein;
transcription regulation; zinc finger eproduct early 21A 24K protein setatus predicted slabel 84K 84K smolecular-veight 28185 schecksum 884

TITLE ORGANISH EVALLETY DATE ACCESSIONS REFERENCE Fauthors cyanobacterium Synechocystis sp. PCC8803. II. Sequence determination of the entire genome and assignment of cross-references MUID: 97051201 eaccession 575510 rr-1997 #sequence_revision 25-Apr-1997 #text_change Dec-1997

T. Sato, S. Kotani, H. Tanaka, A.; Asaminu, E.; mura, Y. Hiyaitaa, N. Hiktopawa, M. Sugiara, M.; moto, S. Kimura, T.; Hosouchi, T.; Matumo, A.; moto, S. Kimura, T.; Hosouchi, T.; Matumo, S.; Ohimpo, K. A.; Makaski, N.; Muro, K.; Okumura, S.; Ohimpo, Takeuchi, C.; Mada, T.; Matanabe, A.; Yamada, M.;

> Page 47 Mon Dec 21 09:28:23 1998

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SUMMARY

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Ouery Match 0.7%; Score 7; DB 2; Length 262; Best Local Similarity 100.0%; Pred. No. 1.04e+01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 142 LEELVAR 148

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Oy 99 LKELVAR 105

ACCESSIONS REFERENCE ORGANISM DATE

aubmitted to the EMBL Data Library, February 1995 G01727 00/17/ etype complete
alpha tocopport transfer protein - human
dformal_name Namo septens #common_name man
21-ber-1990 sequence_revision 06-Jun-1997 #text_change
10-0ct-1997
00/17/2: 52146

preliminary; translated from GB/CMGB/DDBJ
menolecule_upe mRNA,
i=728 **iabbl DEN
i=7

O.7%; Score 7: DB 2: Length 278;
Best Loal Similarity 100.0%; Pred. No. 1.04e+Oi;
Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps ejournal Nature Genet. (1995) 9:141-145
Ataxia with isolated witamin B deficiency is caused by mutations in the alpha-tocopherol transfer protein.
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36 REAGVPL 42 ||||||| 230 REAGVPL 236

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Page 45

Rieger, M., Rivolta, C.: Bocha, E.;
ddie, Y. Satto, T. Scanlon, E.;
R. Scotton, P. Sakiguchi, J.
J. Serror, P. Sakiguchi, J.
J. Serror, P. Shin, B.S.; soldo,
H. Tamakoshi, A.; Takhashi, H.;
H. Tamakoshi, A.; Takhashi, H.;
R.; Toshiyana, S.;
F.; Vasarorti, A.; Valina, S.;
Redler, H.; Heitzeneger, T.;
Vannancto, H.; Vannar, S.; Tasumoto,
A.; Yoshikawa, H.F.; Zunstein, E.;
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# Journal DNA Res. (1996) 31:09-118

# Sequence analysis of the genome of the unicellular

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Blochem, J. (1995) 306:437-44. House alpha-toopperbl transfer protein: cDNA cloning, setStresion and chromosomal localization.
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YULGIGUS
**FORMAL_name Archaeoglobus fulgidus
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Nakamura, Y.; Hiyojima, N.; Hirosaw, M.; Sugitura, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Kuraki, A.; Nakasaki, N.; Matsuo, K.; Okumura, S.; Shimpo,
S.; Taksuchi, C.; Mada, T.; Matanabe, A.; Tanada, K.;
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peptide transport system permease protein SapB · Escherichia
coli (strain K-12)
stormal_name Escherichia coli 17-Sep-1997 stext_change
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attner, F.R.; Plumkett III, G.; Bloch, C.A.; P.
Burland, V.; Rilay, M.; Collado-Vides, J.; Glav
Rode, C.K.; Mayhav, G.F.; Gregor, J.; Davis, N
Virkpatrick, H.A.; Goeden, H.A.; Rose, D.J.; M
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sth, C.I.; McMall, L.K.; Badger, J.H.;
L.; Overbesk, R.; Gocayne, J.D.; Meidan,
L.; Utterbeck, T.; Cotton, M.D.; Spriggs,
Kaline, B.P.; Sykes, S.H.; Sadov, P.M.;
Bownen, C.; Pujil, C.; Gerland, S.A.;
en, G.J.; Fraser, C.M.; Smith, M.O.; Voese,
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Science (1997) 277:1453-1462

Nau, B.; Shao,

Best Local Similarity 100.0h; Pred. No. 1.04+*01; Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ecross-references GB:063541 cell proliferation and tumor COMMENT This protein is involved in cell proliferation and tumor progression. SUBMARY steph 312 schecksum 4470 Query Match 0.71: Score 7: DB 2: Length 342:	*journal Blochem, Blophy». Rea. Commun. (1996) 226:461-466 *title Nolecular cloning of a novel meNA highly sepressed in *contents liver *contents liver *accession po4211 *Brooleculerype mRNA **Freaddumes y 1.342 **slabel RED **Treaddumes y 1.342 **slabel RED		RESULT 40 PC4211 *type fragment EMRY TITLE PC4011 *type fragment PC4010 *type fragment ATERNATE_NAMES NC/NCC protein ATERNATE_NAMES NC/NCC protein ATERNATE_NAMES NC/NCC protein ATERNATE_NAMES NC/NCC protein	Ouery Match 0.74; Score 7; DB 2; Length 339; Best Local Similarity 100.01; Pred. No. 1.04e+01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 287 ASRSLPL 293 01 1111111 09 250 ASRSLPL 356	**************************************	DATE 11-can-1996 sequence_revision 01-Mar-1996 stext_change	9,28,23	Db 83 LAFGPAL 89	Cutry Match 0.7%; Score 7; DB 2; Length 321; Best Local Similarity 100 Oi; Pred. No. 1.040+01; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GENETICS *Gene sap8 *Egene transmembrane protein KEYWORDS transmembrane protein SUBDARY *length J21 *molecular-veight 36083 *checksum 3845	status residues cross-re	•	REQUIT 37 53986 stype complete ENTRY spb protein Salmonella typhamurium ORCHNISH 20cpm.1300 sequence_revision 20-7eb-1995 stext_change DATE 19-50-1900 sequence_revision 20-7eb-1995 stext_change	Dest Local Similarity 100.01; Pred No. 1.04+01; Per	GENETICS **Gene **apB **UNMARY ** elength 321 **molecular-veight 36038 **checksum 1919 **Checksum **1.	**CCCSSION news/ preliminary: nucleic acid sequence not shown: **molecule_type DNA **residues	Stitle The complete genome sequence of Eacherichia coli K-12. scross-references MQID:91416517	Man Dec 21 09:28:23 1998 US-08-951-733-14.zpr
								Page 55	:										Page 53
across-references MG accession 139490 assatus 1	ACCESSIONS 139490 REFERENCE 139490 sauthors De Tro		Db 67 STUTDLQ 73 Oy 786 STUTDLQ 792	smap_position 10L summary slengt Query Match Best Local Similarity Matches 7: Const	authors pohl, authors pohl, accession systy accession \$5679 accession \$5679 accession \$600:ps sgo: ps	ALTERNATE_NAMES hypothem of corner o	OY 236 LGLPAPG 242 RESULT 41 S5679 TITLE hypot	Mon Dec 21 09:28:23 1998		# či	Matches 7: Cons. Db 103 EAGVPLG 109 Db 104 EAGVPLG 117	SUMMARY SUMMARY Query Match Best Local Similarity	##molecule_type ##residues ##cresidues ##cresidues ##cresidues ##cresidues ##cresidues ####################################	of ere	Limm Anno Anno Hobo Chul	ACCESSIONS E69219 REFERENCE A69000 Smith Dubo	RESULT 30 E69219 ENTRY CONSECUTIVE CONSECU	Qy 119 LAFGFAL 125	Mon Dec 21 09:28:23 1998

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Dubola, L.; Daladredge, T.; Bashiradek, M.; Liakely, P.;
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Doola, R.; Dolher, E.; Olarrio, D.; Dedifora, R.; Vecaire, R.;
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Gene (1991) 144:143-14.
Sequence analysis of the Acceptillum brasilense exoS gene,
erence MUZI:3429160
139490 SS5795 *Uppe complete
hypothetical protein Y10023c - yeast (Saccharomyces)
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fformal_name Atceptrillum brasilense
19-Uni-1996 sequence_revision 19-Uni-1996 *text_change
19-Uni-1996 sequence_revision 19-Uni-1996 *text_change
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19490 S16009 \$58158 stype complete hypothetical protein SPAC2P7.14c - fission yeast (Schisosaccharomyces pombe) E89219 *trype complete
conserved hypothetical protein MTH894 - Methanobacterium
thermoautotrophicum (strain Delta H)
sformal_name Methanobacterium thermoautotrophicum
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## residues 1-148 ## stabel RES CENTICS EXCHANGE EXCEPTION CONSTRUCTION FROM THE CALASSIFICATION ## supercasily UDPglucose 4-epi---

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Best Local Similarity 100.0%; Pred. No. 1.04e+01;
Matches 7: Conservative 0: Mismatches 0; Indels 0: Gaps
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saccession I18920 preliminary: tempolecule_type movi
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K.N.: Woodward, D.F.: G.Ll. D.W.
Mol. Pharmacol. (1994) 46:721-720
Chorney of a novel human prostaglandin receptor with Characteristics of the pharmacologically defined EP2 characteristics of the pharmacologically defined EP2
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KEYMORDS ATP; galactok metabolism: phosphotransferase
KEYMORDS ATP; galactok metabolism: phosphotransferase
SUPANRY slength 395 smolecular-weight 40948 schecksum 5698
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submitted to the EMBL Data Library, March 1995
Sequence analysis of the cytochrome b gene of Trimorphomyces
papilionaceus mitochondria.
$5308)
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ubiquinol-cytochromec reductase (EC 1.10.2.2) cytochrome b
- jelly fungus (Trimorphomyces papilionaccus) micochondrion
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Search completed: Fri Dec 18 18:50:22 1998 Job time : 152 secs.

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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd Unit.

Run on: Tabular output MPsrch_pp protein · protein database search, using Smith-Waterman algorithm not Fri Dec 18 18:41:46 1998; generated. MasPar time 23.44 Seconds 1086.892 Million cell updates/sec

Title: Description: Perfect Score: Sequence: Scoring table: >US-08-951-733-14 (1-949) from US08951733.pep 949 1 HASGORCVLLRTWEALADAT TABLE unitprotable Gap 60 HASGORCVLLRTWEALAPAT.....

PVEDEALGGTAFVQMPAHGL 949

Searched: 74019 seqs, 26840295 residues

Post-processing Minimum Match 0% Listing first 1000 summaries

Database: swiss-prot35 l:swissprot

Mean 4.088; Variance 0.405; scale 10.093

Pred. No. is the number of results predicted by chance to l score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution ing printed,

SUMMARIES

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US-08-951-733-14.rsp

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6 0.6 283 1 CEBLIANT AND SETA-1 PR 2.66e-02 131 6 0.6 313 1 MTOLETIC CONTROL FOR CONTROL F	Dec 21 09:23:24 1998 US-08-951-737-14.rsp US-08-951-737-14.rsp US-08-951-737-14.rsp Page 7 Mon Dec 21 09:23:24 1998 100 0.6 279 1 Y818_STWT3 HTPOTHETICAL 30.8 ND P 3.69e+02 257 6 0.6 280 1 DSST_PART DSST_BART 258 0.6 280 1 DSST_PART 259 0.6 280 1 DSST_PART 250	1.55 1.55 1.57

461 60.6 427 1 1131_HMAN INTERLETATI-13 RECEPTO 2.58e+02 463 60.6 429 1 VOO5_MICHA LEVELLA 65.9 TO P. 2.58e+02 463 60.6 429 1 VOO5_MICHA LEVELLA 65.9 TO P. 2.58e+02 463 60.6 429 1 VOO5_MICHA LEVELLA 65.9 TO P. 2.58e+02 465 60.6 430 1 PRAZ_HMAN RE-3-CELL_LEVELIA 78 2.58e+02 465 60.6 430 1 PRAZ_HMAN RE-3-CELL_LEVELIA 78 2.58e+02 467 60.6 430 1 PRAZ_HMAN REDARANGE 78 78 2.58e+02 468 60.6 441 1 PRAZ_HMAN REDARANGE 78 78 2.58e+02 469 60.6 441 1 PRAZ_SCHO TRANSCRIPTIONAL REGULA 2.58e+02 469 60.6 441 1 PRAZ_SCHO TRANSCRIPTIONAL REGULA 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM PRECURE 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM REGER 2.58e+02 469 60.6 444 1 CHAL REMAX PRAZEM REGER 2.58e+02 460 60.6 444 1 CHAL REMAX PRAZEM REGER 2.58e+02 460 60.6 444 1 CHAL REMAX PRAZEM REGER 2.58e+02 460 60.6 444 1 CHAL REMAX PRAZEM REGER 2.58e+02 460 60.6 444 1 CHAL REMAX PRAZEM REGER 2.58e+02 460 60.6 445 1 CHAL REMAX PRAZEM REGER 2.58e+02 460 60.6 445 1 CHAL RE	Mon Dec 21 09:28:24 1998 US-08-951-733-14.rep	359 6 0.6 349 1 YAYS_TRAST HYDOTRETICAL 40.3 ND P 2.59e-02 350 6 0.6 350 1 HCLL_HYDAN HYDOTRETICAL 30.5 ND P 2.59e-02 351 6 0.6 350 1 HCLL_HYDAN HYDOTRETICAL 30.5 ND P 2.59e-02 352 6 0.6 350 1 HCLL_HYDAN HYDOTRETICAL 30.5 ND P 2.59e-02 353 6 0.6 350 1 HCLL_HYDAN HYDOTRETICAL 30.5 ND P 2.59e-02 354 6 0.6 351 1 HERE_ALCHU HYDROGRAGE_EXPENSION 2.59e-02 355 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 356 0 0.6 355 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 357 6 0.6 355 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 358 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 359 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 350 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 350 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 351 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 352 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 353 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 354 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 355 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 356 0.6 350 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 357 6 0.6 350 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 358 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 359 1 HAS_AND HYDROGRAGE_EXPENSION 2.59e-02 350 1 HAS_AND HYDROGRAGE_EXPAIN C.39e-02 350 1 HAS_AND HYDROGRAGE_EXPAIN C.3	Non Dec 21 09:28:24 1998 US-08-951-733-14.rep	•
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	Page 15		Page 13
116 6 6.79 1 ITHQ_EDOLI HTPOTHETICAL 77.3 KD P 2.59+02 117. 6 0.6 6859 1 ANTI_CLEMAN REPRESENTATE REPRESENTATION PROTECTION PROTE	Mon Dec 21 09:28:24 1998 US-08-951-733-14.rsp	\$13.0 G. S. S. G. G. S. S. G. G	Mon Dec 21 09:28:24 1998 US-08-951-733-14.zep

869 6 0.6 1002 1 2005.CHICK ENRIN TIPE-B RECEPTOR 2 : 504-02 877 6 0.6 1003 1 DOC_CHEME DATCH_TAMA SITIENTESS 2 : 504-02 878 6 0.6 1003 1 DOC_CHEME DATCH_TAMA SITIENTESS 2 : 504-02 879 6 0.6 1003 1 DOC_CHEME DATCH_TAMA SITIENTESS 2 : 504-02 879 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 879 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 879 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 879 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 879 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 870 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 870 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 871 6 0.6 1003 1 CAPL_DEPON BOUNDESS 2 : 504-02 872 6 0.6 1003 1 SPT_LESS 1 CAPL_DEPON BOUNDESS 2 : 504-02 873 6 0.6 1003 1 SPT_LESS 1 CAPL_DEPON BOUNDESS 2 : 504-02 874 6 0.6 1003 1 SPT_LESS 2 : 504-02 875 6 0.	Mon Dec 21 09:28:24 1998 US-08-951-733-14.xep	767 768 769 769 760 760 760 761 776 776 777 777 777 777 777 777 777	t Mon Dec 21 09:28:24 1998 US-08-951-733-14.xmp
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0.6 1431 DAPK_HDMA DEACH-ASSOCIATED PROTE 2.68e-02 221 6 0.6 14431 SEEP_ANGES MACHINEPERILARS PROTE 2.68e-02 222 6 0.6 14461 INTERPROTE AND PROTEIN FARE 2.68e-02 223 6 0.6 14651 INTERPROTEIN FARE 2.68e-02 224 6 0.6 14651 INTERPROTEIN FARE 2.68e-02 225 6 0.6 14651 INTERPROTEIN FARE 2.68e-02 226 6 0.6 14651 INTERPROTEIN FARE 2.68e-02 227 6 0.6 14651 INTERPROTEIN FARE 2	Mon Dec 21 09:28:24 1998 US-08-951-733-14.zep	### 6 0.6 831 1 41_FUMAN PROTEIN 4.1 (BAND 4.1) 2.59e-02 ### 6 0.6 835 1 CCC48 PAST CELL DIVENSION CONTROL ### 6 0.6 835 1 CCC48 PAST CELL DIVENSION CONTROL ### 6 0.6 835 1 CCC48 PAST CELL DIVENSION CONTROL ### 6 0.6 836 1 CCC48 PAST CELL DIVENSION CONTROL ### 6 0.6 836 1 CCC48 PAST CELL DIVENSION CONTROL ### 6 0.6 836 1 CCC48 PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON ### 6 0.6 836 1 CCC48 PAST PAST CELCOPROTEIN FRANCISCON #	Mon Dac 21 09:28:24 1998 US-08-951-733-14-Xap
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SEQUENCE OF 10-124 FROM N.A.
TISSUB-T-CEIL;
KEDLINE: 8604365.
SHEN F.-H., SAGA Y., LITMAN G., FREEMAN G., TUNG
BOYSE E.A.;
PROC. NATL. ACAD. SCI. U.S.A. 82:7360-7363(1985).
[4]

TUNG J.-S.,

ZZI REVISIONS SAGA Y., TUNC J.-S., SHEN F.-W., BOYSE E.A.; PROC. NATL. ACAD. SCI. U.S.A. 84:1991-1991(1987). [3]

ALIGNMENTS

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TOA4. JOURE STANDARD: PRT; 1152 AA.

101.JAN-1988 (REL. 06, CREATED)

101.JAN-1988 (REL. 06, CREATED)

101.HOW-1989 (REL. 05, LAST SECURACE UPDATE)

101.HOW-1989 (REL. 35, LAST ANECTATION UPDATE)

LYPHROCITE COMPONEN AUTICEN LY-5 PRECURSOR (EC 3.1.3.48) (200 ED TSOPORM) (CD45) (T200).

TOPROCI (T200).

TORRESULUS (MOUSE).

UPLANE (TARROTA). RETERLON; CHORDATA; VERTERNATA; TETRAPODA; MAMMALIA;

UPLANE (TARROTA). RETERLON; CHORDATA; VERTERNATA; TETRAPODA; MAMMALIA;

LITHERIAA, RODENTIA.
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MEDLINE; 8631366.

SACA Y. TUGO J.-S. SHEN F.-W., BOYSE E.A.;

PROC. NATL. ACAD. SCI. U.S.A. 83:6940-6944(1986).
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PROTEIN-TIROSINE PHOSPHATASE.

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RP SEQUENCE OF 832-1152 FROM N.A.

RE KEDLINE; 87092355.

RA MASCHEM PG.

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1998
US-08-951-733-14.rap
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EXOTENCE FROM W.A.

EXECUTE: 87040763 M.A.

EXECUTE: 87040763 M.A.

EXECUTE: 87040763 M.A.

EXECUTE: 8074076 M.A.

EXECUTE: 8074077 M.A.

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                                  Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              UNC_VEVD STANDARD: PRT: 305 AA.
P09307;
01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST EGODENCE UPDATE)
15-7UT-1989 (REL. 36, LAST ANOCATION UPDATE)
URACII-DNA GIZCOSYLASE (EC 3.2.2.-) (UDG).
                         SECURENCE PROM N.A.
MEDLINE: 8506657.

J. GRN. VIROL. 67:1759-1816(1986).

J. GRN. VIROL. 67:1759-1816(1986).

H. FUNCTION: EXCUSES URACII. RESIDUES FROM THE DRA WHICH CAN ARISE

H. FUNCTION: EXCUSES URACII. RESIDUES FROM THE DRA WHICH CAN ARISE

A RESULT OF MISSINGENERAL PROPERTY OF CUTTOSINE. DRA

POLIFIENSE OR DUTE TO DEMAINATION OF CUTTOSINE. PAMILY.

PERL. 704370, GEOORS TO THE URACII.-DNA GLYCOSTIASE FAMILY.

PROSITE: PS00110; U.DNA_GLYCOSTIASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 EEEDTDPR 59
||||||||||||
461 EEEDTDPR 468
                                                                                                                                                                                                                                                                                                                                             VARICELIA-ZOSTER VIRUS (STRAIN DUWAS) (VZV).
VIRIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8; DB 1; Length 155;
Pred. No. 3.48e-02;
0; Mismatches 0; Indels
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0 Caps 0

(PRACHEN) PREMAZA. PREMAZA. EURASCOA, EPIGA. EUTREKIA; ARTIODACTIA. EUTREKIA; ARTIODACTIA.

MAMMALIA; CHAIN

ALPHAHERPESVIRINAE

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8 LAPGFALLD 16 ||||||||| 119 LAPGFALLD 127

RAP2_PIG P05207; 13-AUG-1987 (REI 13-AUG-1987 (REI 01-FEB-1996 (REI CAMP-DEPENDENTI

STANDARD;

PRT;

(REL. 05, CREATED) (REL. 05, LAST SEDUENCE UPDATE) (REL. 33, LAST ANNORATION UPDATE) DNT PROTEIN KINASE TYPE II-ALPHA REGULATORY

Query Match 0.9%; Best Local Similarity 100.0%; Matches 9; Conservative

Score 9; DB 1; Length 1152; Pred. No. 1.50e-04; 0; Mismatches 0; Indels

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Gaps

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DNA REPAIR: HYDBOLASE; GLYCOSIDASE,
ACT_SITE 148 6148; GENERAL BASE (BY SIMILARITY)
SEQUENCE 305 AA; 34376 M4; DDD3564F CRC32;
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Query Match 0.8%; Score 8; DB 1; Length 305; Best Local Similarity 100 0%; Pred. No. 3.48e-02; Matches 8; Conservative 0; Mismatches 0; Indels 0

0

231 RVLQRLCE 238 ||||||| 105 RVLQRLCE 112

TROS_MOVES STANDARD: PRT: 342 AA.

10.1411:
10.1 (REA/TED)
10.1 (ARR-1999 (REL. 10, CREA/TED)
10.1 (ARR-1999 (REL. 10, LAST ANDOTATION UDDATE)
10.1 (ROY-1995 (REL. 32, LAST ANDOTATION UDDATE)
MOS RESTRET/THENDENIE-PROTEIN RILASE TRANSFORMING PROTEIN (EC 2.7.1.-).

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FRIEL J., STOCKING C., STACEY A., OSTERTAG W.; J. VIROL. 61:808-987 (1987). - I- SIMILARITY: MITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-

D) STRUCTURE MODILING.

MEDLING, 875585

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THE STRUCTURE A. B. BESS J., TAXLOR S.S.;

BICCHEMISTRY JS. 343-351 (997) D. THE ENERGY S. COMPOSED OF TWO

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THE STRUCTURE CHAINS ME DOWN CAMPAINTIC CHAINS AND A REGULATORY DIMERS

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MODIFICATION OF THE STRUCTURE AND IN OTHERS

SEODERKE. TISSUE-HEART MUSCLE; TAKIO K., SKITH S.B., KREBS E.G., WALSH K.A., TITANI TAKIO K., SKITH S.B., KREBS E.G., WALSH K.A., TITANI PROC. MATL. MCAD. SCI. U.S.A. 79:2544-2548(1982). PROC. MATL. MCAD. SCI. U.S.A. 79:2544-2548(1982).

11-VII-1986 (REL. 01. CREATED)
21-VII-1986 (REL. 01. LAST ENQUENCE UPDATE)
01-FEB-1996 (REL. 33; LAST ANNOTATION UPDATE)
CAMP-DEPENDERT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN.
FRANCALA.
BOS TAURUS (BOVIIE). CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA;
EUTHARTOTA; METARON, CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA;
EUTHARTOTA; METARON, CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA;

STANDARD;

PRT;

400 AA

211.

DOMAIN 63 3
NP_BIND 69
BINDING 90
ACT_SITE 198 1
SEQUENCE 342 AA; PROSITE, PSOULOT, PROTEIN KINSE, ATP. 1.
PROSITE, PSOULD PROTEIN KINSE, PT. 1.
PROSITE, PSOULD PROTEIN KINSE, DOM. 1.
PRANSFERARE, SERINE/THRONTHE PROTEIN KINSE; ONCOGENE,
TPANSFERARE, SERINE/THRONTHE PROTEIN KINSE; ONCOGENE,
TPANSFERARE, PROTEIN KINSE; ONCOGENE,
TPANSFERARE, PROTEIN KINSE; ONCOGENE, 338 P 77 A 90 A 198 B 198 B PROTEIN KIMASE.
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AIP (BY SIMILARITY).
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MM; 1066243C CRC32;

Query Match 0.8%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8: DB 1: Length 342; Pred. No. 3.48e-02; 0; Mismatches 0; Indels ő Caps

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291 LRPSLTGA 298 ||||||| 372 LRPSLTGA 379

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BINDING 343 BINDING 343 SEQUENCE 400 AA; 44962 MW; CAMP. CAMP. ; 1F7A0D99 CRC32;

Query Match 0.83; Score 8; DB 1; Length 400; Best Local Similarity 100.03; Pred. No. 3, 48e-02; Matches 8; Conservative 0; Mismatches 0; Indels 0; Indels 0; Caps 0

106 EEEDTDPR 113 |||||||| 461 EEEDTDPR 468

ANPA_EURAN STANDARD: PRT: 403 AA.
PA1951: 016801; 13. CREATED)
01-JAN-1990 (REL. 13. LAST ENGUENCE UPDATE)
01-JAN-1990 (REL. 13. LAST ENGUENCE UPDATE)
15-JUL-1998 (REL. 15. LAST ANNOTATION UPDATE)
CAMP-DEPENDERT PROFIEM KINASE TYPE II-ALFHR REGULATORY CHAIN.
PRAMAZIA ON PREZ OR PRAMAZI.
EDNO SAPIEMS (HUTAH): MOREONATA: VERTESHATA: TETRAPODA: MAMALIA:
INTHERATA: PHIMATES.

EQUENCE FROM N.A.

MEDLINE: 89211413. OYEN O., MYKLEBUST F., SCOTT J.D., PEBS LETT. 246:57-64(1989). HANSSON V., JAHNSEN T.;

RY SECURNCE OF 1-05 FROM N.A.

RY SECURING 9 1010ES R. SIMARD J., MTKLEDUST F., RANSSON V.,

RA DOSE HTD 9 1010ESC R., SIMARD J., MTKLEDUST F., RANSSON V.,

RA DOSE HTD 9 1010ESC R., SIMARD J., MTKLEDUST F., RANSSON V.,

RA DOCHIM SIOPHYS ACTA 1150:89-106(1997).

RE DIOCHIM SIOPHYS ACTA 1150:89-106(1997).

RE DIOCHIM SIOPHYS ACTA 1150:89-106 POTESTA PROPERTY.

CC 1 FINCTION TOP IN ESCULATOR CHAINS ACCITATION OF THE MAPP SITE SOMPOSED OF TWO

CC 1 SISBUILT: THE INCITIVE NORMATICA CHAINS. ACTIVATION PACKED

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CC 1 TISSUES TRO ACTIVE CAPALITIC CHONORS AND IN SULLATORY OF THE MAPP SITE SPECIFICATIVE FOR TYPES OF REGULATORY CHAINS ARE POUND:

CC 1 TISSUES TRO SITE SITE OF THE ACTIVATED CATALITIC CHAIN.

CR 1 PROCEDURATED BY THE ACTIVATED CATALITIC CHAIN.

DR 1859, POOSIS; JAPK.

DR 1859, POOSIS; JAPK.

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ACETTLATION.
PHOSPHORILATION (BY ACTIVATED ENSINE)
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COMP_BINDING_1: 2. COMP_BINDING_3: 2. COMP_BINDING_3: 2. SPHORYLATION: DUPLICATION; MULTIGENE FAMILY:

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Query Match 0.8%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 403; Pred. No. 3.48e-02; 0; Mismatches 0; Indels 0

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HEST, YEAST STANDARD; PRT: 654 AA.

PIJ198.

01-007-1999 (REL. 12, CREATED)
01-007-1999 (REL. 12, LAST ANDOTATION UDDATE)
01-007-1999 (REL. 14, LAST ANDOTATION UDDATE)
KITOCHOMBRIAL HEAT SHOOT REOTERS SCI PRECURSOR (ENDORUCLEASE SCEI OS DUBUNIT).

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SACCHAROMYCES CERETISIAE (BRAKE & YEAST).

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STRAIN-DOID-10B.
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STRAIN-DOID-10B.
CRAIG E.A., RAMARE J., SHILLING J., WENNER-WASHBURNE H., HOLMES S.,
KOSIC-SHITHERS J., NUCOLET C.H.,
MOLI-CELL BIOL. 9.1000-1006(1989).

SEGUENCE FROM N.A., AND SEQUENCE OF 24-41. STRAIN-IAM 4274: MEDLINE: 90368701.

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MORISHIMA N., NAKAGAWA K., YAMAMOTO E., SHIBATA T.; 1. BIOL. CHEM. 265:15189-15197(1990).

ENGUENCE PROM N.A. TRAIN-5286; ERDLINE; 9139759; TUANG M.-B. CHUNT J.-C., GALIBERT F.; PAST 11:775-781(1995).

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TERD, 6692; ...
TERD, 8704; ...
TERD, 8704; ...
TERD, 8704; ...
SGD; LODONSAI, SECI.
PROSITE: PSO029; HEF70_1; 1.
PROSITE: PS0029; HEF70_2; 1.
PROSITE: PS002; AFP-BINDING; MULTGENE PAMILY; MITOCHONDRION;
TRANSIT PEPTIE: 1
23 HITOCHONDRION.
TRANSIT PEPTIE: 1
24 654 HEAT SHOUR PROFITE SECI.

ENDURING OF 24-18.

REDLIES. 9103254.

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CHERES P. B. STARLEG U.C., HMANG S.T., VESTMERER D., SCHATE G.,

REDLO J. 9.4115.4122(1980)

- PURCTION: SCL. 19 AM SESSMENTIAL MITCOHONDRIAL PROFESIN.

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238 LPAPGARR 245
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SEQUENCE 968 AA; 111485 MW; 53CE3BE2 CRC32;
                                                                                                                                                                   SEQUENCE 1480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 09:28:24
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BONO SAPIENS (HUMAN).
EZMANICTA, METAGOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EZMHERIA; PRIMATES.
EXTHERIA; PRIMATES.
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001969; 015684;
001-UL-1993 (REL. 26, CREATED)
01-UL-1993 (REL. 26, LAST SEQUENCE UPDATE)
11-UL-1998 (REL. 36, LAST NEUTRICON UPDATE)
12-UL-1998 (REL. 36, LAST NEUTRICON UPDATE)
COMPACT S
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ISSUE-KIDNEY.
TEREE O., OLVOS I H., OKABE I., BAILEY L.C., NELSON D.L.,
FRIES R.A., MIINNES R.E., MUSSBAUN R.L.;
AVUEZ 356:334-43(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE OF 491-968 FROM N.A.
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Pred. No. 3.48e-02;
0; Mismatches 0; Indels
                                                 Score 8; DB 1; Leng
Pred. No. 3.48e-02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1480 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-951-733-14.rsp
                                                      Indels
                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                      Caps
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973521;
01-077-1993 (REL. 27, CREATED)
01-077-1993 (REL. 13, LAST SEQUENCE UPDATE)
01-807-1997 (REL. 35, LAST ANNOTATION UPDATE)
PART PROTEIN ADP3 OR YIROGG OR YIBGC.
PART OR HIP3 OR HDP3 OR YIROGG OR YIBGC.
PART OR HEP3 OR HDP3 OR YIROGG OR YIBGC.
PART OR HEP3 OR HDP3 OR YIROGG OR YIBGC.
PART OR HEP3 OR HDP3 OR YIROGG OR YIBGC.
PART OR HDP3 OR YIROGG OR YIBGC.

片

595 LKELVARV 602 ||||||| 99 LKELVARV 106

Query Match 0.8%; Best Local Similarity 100.0%; Matches 8; Conservative

Score 8; DB 1; Length 654; Pred. No. 3.48e-02; 0; Mismatches 0; Indels

0 Caps 0 634 643 650 654 **M**;

23 E 654 E 646 E 643 E 650 E

MITOCHONDRION
HEAT SHOCK PROTEIN SSC1.
ASSW-RICH.
ASSW-RICH.
N > NN (IN REF. 2).
G -> D (IN REF. 2).
MY: OEB32F62 CRC32;

STRAINSSEC, PROM H A.

STRAINSSEC, JASCIZ.

STRAINSSEC, JASCIZ.

STRAINSSEC, JASCIZ.

BARRELL B.C. BALDCOR.

CURRELER C.J., LOUNG R., CONSET T., DEAR S., DETLIN K., FRASER A.,

CURRELER C.J., LOUNG R., CONSELT T., DEAR S., JACELS K., CONES M.,

LOUIS S., HAMICH NOT. BORSHELL T.S., DETLIC C., PRASEO D.,

DOILS S., LOUIS T., DETLIC T., SELUCHO J., SHITTH V.,

WANDRAM M., TERLES L., BOWLET M., SELUCHO J., SHITTH V.,

WHAT SELUCION S. JACKS C. SELUCTOR JATA BANKS.

ACHS A.B., DEARDORFF J.A.; ELL 70:961-973(1992).

EQUENCE FROM N.A., AND SEQUENCE OF 320-344; 352-375 AND 899-906.

BE A SUBUNIT

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175 175 199 199 199 199 199 199

15 X 12 AA APPROXIMATE REPEATS.
1-1.
1-2.
1-3.
1-4.
1-5.
1-7.

AES J., TEODORU C., VALENCIA A., SENSEN C., WIEMANN S., IMMERIAANN J., SANDER C., ANSORGE W.;

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Mon
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RESULT 11

ID MICHAEL MOUSE
AC P09541;
DT 01-MAR-1989 ()
DT 01-PEB-1991 ()
DT 01-PEB-1996 ()
DT MYOSIN LIGHT ()
       ₹ ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCES
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NEW SENDENCE, 92109716

NEW COLLEGAN M. E., PAN Y. C. C., ETHERTON T. D.;

NOCHCHA, BIOCHTER, RES. CONDUN, 181:1111-1116(1991).

RL BIOCHEM, BIOCHTER, RES. CONDUN, 181:1111-1116(1991).

RL BIOCHEM, BIOCHTER, RES. CONDUN, 181:1111-1116, RESTELLATE, RIEL GROWTH

CC. INTERACTION OF THE SIGN SHIP THERE RELL GREEN PROPOSE.

CC. INTERACTION OF THE SIGN SHIP THERE RELL SURFACE RECEPTORS.

CC. INTERACTION OF THE NOTE THAN 1GP-1.

CC. INTERACTION BIOCHTER NOTE THE RECEPTORS.

CC. INTERACTION OF THE INSULIN-LIKE GROWTH FACTOR BINDING CONTROL SURFACE RECEPTORS.

CC. INTERACTION SHIP THE STATEMENT OF THE INSULIN-LIKE GROWTH FACTOR BINDING CONTROL SURFACE RESERVED.

CC. INTERACTION SHIP THE STATEMENT OF THE INSULIN-LIKE GROWTH FACTOR BINDING CONTROL SHIP PROCESSES AND THE SHIP PROPOSED SHIP PROCESSES AND THE SHIP PROPOSED AND THE SHIP PROCESSES AND THE SHIP PROCESSES AND THE SHIP PROPOSED AND THE SHIP PROCESSES AND THE SHIP PR
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                                                                                                                                                                                                                                                                                    Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PER: A02016; RWHUTA.

HSSP: PO1607; HHTL.

T-CELL: RECEPTOR GLICOPPOTEIN: SIGNAL.

SIGNAL PARTICLES TO T-CELL RECEPTOR GLICOPPOTEIN: SIGNAL.

1000A.N 28 139 7-CELL RECEPT.

DOMALN 111 115 D SEGMENT.

DOMALN 112 115 D SEGMENT.

DOMALN 115 139 J SEGMENT.

DISCUENT 19 116

ROW, TER 119 119

SECUENCE 139 AA: 15441 MM; SEAE2341 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Opery Match 0,7%; Score 7; DB 1; Length 23; Best Local Similarity 100.0%; Pred. No. 4.76+00; Indels Matches 7; Conservative 0; Mismatches 0; Indels
21 09:28:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUS SCROFA (PIG).
EUNARYOTA, METASOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUVHERIA; ARTIODACTIA.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SOCJUKCE UPDATE)
01-FEB-1996 (REL. 3) LAST ANNOZATION UPDATE)
101-GRULPH-LIKE GROWTH PACTOR BINDLING PROTEIN 3 (1GPB)
110-FEB-1991 (PRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 LLGASVL 10
|||||||
697 LLGASVL 703
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINS-C:
REDLINE: 93204900.
ROPER D.I., FANCETT T., COOPER R.A.;
ROL. GEN. GENET. 237:241-250(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 RPPPAAP 21
|||||||
| 85 RPPPAAP 91
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121 125
126 139
139 139
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(REL. 17, LAST SEQUENCE UPDATE)
(REL. 13, LAST ANNOTATION UPDATE)
T CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7: DB 1; Length 139;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-CELL RECEPTOR ALPHA CHAIN V REGION V SECHENT.
D SECHENT.
J SEGMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8EAE2341 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IGFBP-2)
                                                                                                                                                                                                                                                                                                          ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IBP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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M
    RESULT
ID RI
AC P7.
OI 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dec
  RISB_MCCTU STANDARD; PRT; 154 AA.
P71655; CTU STANDARD; PRT; 154 AA.
P71655; CTU STANDARD; PRT; 154 AA.
P71657; CREL. 35 LAST ARROTATION DEPART)
01.NOV-1997 (REL. 35 LAST ARROTATION DEPART)
6,7-DINTERT-8-RESITTLLOHALITE STRUMASE (DE 3.5.1.8) (DMRL
LUDMALIE STRUMASE) (RISOTAVIM STRUMASE BETA CHAIN).
                                                                                                                                                                27 RGAKNYL 33
|||||||
113 RGAKNYL 119
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TE TYAL_PHONAN STANDARD; PRT: 139 AA.

AC PO4437;
DT 13-AGC-1987 (REL. 05, CREATED)
DT 13-AGC-1987 (REL. 05, CREATED)
DT 13-AGC-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).
DE 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).
DE 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).
DE 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).
DE 211ANTONA, METAMONA, CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DE 211ANTONA PRIMATES.
RN SEQUENCE FROM N.A.
RX EDILHE, 86378770.
RA LEIDEN J.M. FRASER J.D., STRONINGER J.L.;
RI IMMUNOCEMETICS 34:17-21(1986).
RI IMMUNOCEMETICS 34:17-21(1986).
RI IMMUNOCEMETICS 34:17-21(1986).
DE 211ANTES SEQUENCE WAS DESIVED FROM A RUMAN CYTOTOXIC T-LYMPHOCYTE
DN 286EL; M15565; 039676; ...
                                                                                                           RESULT 14

ID TOLLAMICTU STANDARD: PRI; 153 AA.

AC 010330; 1996 (REL. 14, CREATED)

DI 01-00711996 (REL. 34, LAST SOUTHER UPDATE)

DI 01-00711996 (REL. 34, LAST SOUTHER UPDATE)

DI 01-00711996 (REL. 34, LAST SOUTHER)

DI MITOLICIELLA 18.8 ED PROTEIN CT497.1.9C.

ON MITOLICIELLA 18.8 ED PROTEIN CT497.1.9C.

ON MITOLICIELLA 19.8 IN DEPORTE AND MITOLICIEL PROTEIN

RE SOUTHER 1. MARSIS D., BARRELL B.G., BALANDREAM N. R. SERNITED (APR-1996) TO EMPLOYERANT/DOBS DATA B. C. 1- SHILLANTE ELECNIS TO THE AND-CTAN FAMILY.

DR MEDI: 200631 E235199: -

NEW MITOLICIELLA 19.5 IN THE AND-CTAN FAMILY.

DR MEDI: 200631 E235199: -

NEW MITOLICIELLA 19.5 IN THE AND-CTAN FAMILY.

DR MEDI: 200631 E235199: -

NEW MITOLICIELLA 19.5 IN THE AND-CTAN FAMILY.

DR MEDI: 200631 E235199: -

NEW MITOLICIELLA 19.5 IN THE AND-CTAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RE SETULINCAIR TISCUE-SPEERN;
RR MEDICINE; 89037447.
RA COMEN A. DARTON P. JAR., ROBERT B., GARNER I., ALONSO S.,
RA GUCIENCA M. E.;
RA SUCLIEC ACTOS RES. 16:10037-10052(1988).
RC -1- STRUMIT: MYOSIN IS AN MEXAMER OF 2 HANY CHAINS & 4 LIGHT CHAINS.
CC -1- SHILMAITI: TO OTHER EF-HAND CALCIUM SHMDIMG PROTEINS, BUT THIS
CC PROTEIN DOES NOT BIND CALCIUM.
PROTEIN DOES NOT BIND CALCIUM.
RESELVATIONS: 030443.
ROBERT MOSILE PROTEIN, MULTIGENE FAMILY.
RESELVATIONS: 1005216 PROTEIN, MULTIGENE FAMILY.
RT 1003. TERM 51 14. 5085 MW; 4ECJAC9B CRC12;
Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S30280; S30280,
PROSITE; PS0111; HTH_MARR_FAMILY; 1.
TANACRIPTION RECUMATION; REPRESSOR: DNA-BINDING.
SEQUENCE 148 AA; 17255 MN; A4EOAAE6 CRC32;
                                                                                                           SEQUENCE FROM N.A.

STRAIN-BJ/RW;

LTER K., BARRIS D., BARRELL B.G., RAJANDREAM
OLYER K., BARRIS D., BARRELL B.G., RAJANDREAM
SUBMITED (APR-1996) TO ENGLY/CERNAKK, DUBJ DATA
-1- SIMILARITE BELONGS TO THE AHPC/TSA FAMILY.
ENGL, 170691; B233309;

SEQUENCE 133 AA: 16819 NH; OPD30CFC CRC31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AAPEPER 39
|||||||
264 AAPEPER 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECURACE FROM H.

KEDLINE: 68736770

LEZIDEN J. K., FRASER J. D., STRONINGER J.L.;

LEGIDEN J. K., FRASER J. D., STRONINGER J.L.;

LEGIDEN J. K., FRASER J. D., STRONINGER J.L.;

LEGIDEN J. K., FRASER J. D., STRONINGER J.L.;

EMBL. MISSES: GJ38768; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FPAGGETT).
MYL3 OR MCLIV.
MUS MUSCULUS (MOUSE).
EUTHERYOTH, METALOA, CHORDATA; VERTEBRATA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1/1/1/1/1
372 LRPSLTG 378
                                                                                                                                                                                                                                                                                                                                                                                       MICOBACTERIUM TUBERCULOSIS.
ROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 LRPSLTG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7: DB 1: Length 148;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
        Score 7; DB 1; Length 153;
Pred. No. 4.47e+00;
0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 1; Length 51;
Pred. No. 4.47e+00;
O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-951-733-14.rsp
                                                                                                                                                                                                                                   BANKS
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RIBH OR MTCY2184.34. MYCOBACTERIUM TUBERCULOSIS. PROXARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE

US-08-951-733-14.rsp

Page 37

Dec 21 09:28:24 1998

SEQUENCE FROM N.A. STRAIN-H37RV:

MUNITED D. MARIEL D., BARRELL B.C., DAIANDREM M.A.

SUBSTITE D. DESCLOSION PROCESSION MARIESTA DE MUNITED DE MUNICIPAL DEL MUNICIPAL DE MUNICIPAL DE MUNICIPAL DEL MUNICIPAL DEL MUNICIPAL DEL MUNICIPAL DEL MUNICIPAL DEL MUNICIPAL DEL MUNICI

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative 28 ALLDGAR 34 ||||||| 124 ALLDGAR 130 Score 7; DB 1; Length 154; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

Indels ő

Gaps

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RR7_SPIAC STANDARD; PRT; 155 AA.
P47374;
01-MOV-1995 (REL. 32, CREATED)
01-MOV-1995 (REL. 32, LAST REQUERCE UPDATE)
01-PES-1996 (REL. 33, LAST REQUERCE UPDATE)
01-PES-1996 (REL. 33, LAST REQUERCE UPDATE)
REQUERCE OF REPOSEMAL PROTEIN S7.

SPIROGYRA MAXIMA. CHLOROPLAST.

EUKARYOTA: PLANTA; PHYCOPHYTA; CHLOROPHYTA (GREEN ALGAE); CONJUGATOPHYCEAE; EYGNEMATALES; EYGNEMATINEAE; EYGNEMATACEAE

EQUENCE PROM N.A. EW K.A., MANHART J.R.; PHYCOL. 29:500-505(1993).

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YOPQ_YEREN P27474; 01-AUG-1992 01-AUG-1992

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STANDARD; PRT; 182 AA

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Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 182; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

0

Gaps 0

CANCE.1993 (REL. 23, CREATE).
01-MG.1993 (REL. 23, CREATE).
01-MG.1993 (REL. 23, LAST BEQUENCE UPDATE).
10-MG.1993 (REL. 26, LAST ANNOTATION UPDATE).
10-MG. DROZELN PAECUESOR.
10-MG. DROZELN PAECUESOR

62 GSILSTL 68 ||||||| || 856 GSILSTL 862

RESULT 19
ID MLEY_RAT STANDARD; PRT; 199 AA.
AC 916409; AC 916409
DT 01-AGC-1990 (REL. 15, CREATED)
DT 01-AGC-1990 (REL. 15, LAST SECRETED UPDATE)
DT 01-FEB-1996 (REL. 31, LAST SECRETED UPDATE)
DT 01-FEB-1996 (REL. 31, LAST SECRETATION UPDATE)
DT 01-AGC-1990 (REL. 31, LAST SECRETATION UPDATE)
DT 01-FEB-1996 (REL. 31, LAST SECRETATION UPDATE)
DT

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SEQUENCE FROM N.A.
TISSUE-HEART VENTRICLE;
HEDLINE: 8924031.
HEDLINE: 8924001.
HCNALLY E., BUTTRICK P., LEINWAND L.;

SEQUENCE FROM N.A.
STRAIN-WISTAR, TISSUE-HEART VENTRICLE;
MEDLINE; 90016857.
PERIASANY M., WODGAONKAR R., KUMAR C.,

PRILLAGIZ NU'RED'ALONDAR, R., KUMAR C., MARTIN B.J., SIDDIQUI M.A.Q.;

RUNGUZZO ALUEN ERES, 17.731-7794.1981), DENTON G. 4 LIGHT CHAINS.

C. --- SUBLINIT, MYCHEN ET-AMPC OF J HEAVY CHAINS. 4 LIGHT CHAINS.

CC --- PROTEIN DOES NOT BIND CALCIUM.

PROTEIN SOES NOT BIND CALCIUM.

REBLI, X145225, G763179; --
DR EMEL, X145215, G763179; --
DR EMEL, X1

SEQUENCE 199 AA; 22025 MW; 0426BB63 CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 199; Pred. No. 4.47e+00; 0; Mismatches 0; Indels 0

29 AAPEPER 35 ||||||| 264 AAPEPER 270

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RESULT
AC PSECUT
DT 01
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RESULT
RESU TEGL_CAREL STANDARD: PRT; 257 AA.
P55336; 039405;
01-007-1996 (REL. 34, CREATED)
01-007-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANOVATION UPDATE)
11707HETICAL 28:7 EN PROTEIN F13E6.1 IN CHROMOSOME X.
12186-13. DITIAL ELECANS.
12186-13. METIADA: ACOSLOMATES: NEMATODA: SECENNENTEA: RHABDITIDA.

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-1- SHILARITY: BELONGS TO THE 87P PANILY OF RIBGEONAL PROTEINS.

BOIL, LO7933; CA170153:
PROSITE: PS00052; BIBGEONAL_97; 1.
RIBGEONAL PROTEIN, CELEDROMALST:
SEQUENCE 155 AA; 17769 MY: 6958C1AB CBC32;

8**2**2228

Query Match 0.7%; Score 7; DB 1; Length 155; Best Local Similarity 100.0%; Pred. No. 4.47e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0 Gaps

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77 ARRRGGS 83 |||||||| 243 ARRRGGS 249

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ILT 17

EUVC_PEAR STANDARD; PRT; 174 AA.

G5.124;
G5.124;
G1.180*.1997 (REL. 35, CREATED)
G1.180*.1997 (REL. 35, LAST SEQUENCE UPDATE)
G1.180*.1997 (REL. 35, LAST SEQUENCE UPDATE)
G1.180*.1997 (REL. 35, LAST ANNOTATION UPDATE)
GROSSOVER JUNCTION HUGLEASE RUVC) (ROLLIDAY JUNCTION RESOLVASE RUVC).

ROUL:

REPUBLICATION HUGLEASE RUVC) (ROLLIDAY JUNCTION RESOLVASE RUVC).

PREVIDENDAS ARRIGIANSA.
PROMARIOTA, GRACILICUTES; SCOTOBACTERIA; AZROBIC RODS AND COCCI;
PSEUDOMORADACEAE.

RE SEQUENCE FROM N.A.

RE STRAILF-RALL:

REST STRA

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 174; Pred. No. 4.47e+00; 0; Mismatches 0; Indels 6

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MAGGENGON S.;

SUBMITTED (NOW-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

FIG. STALLARITY: TO EMDAN PROTEIN D52.

EMBL. 568105; C0072144;

WORDTEN; F1185.1: CE03198.

SEDQUENCE 257 AA; 28696 MM; 66FDB900 CRC32;
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VARSPLIC 164
VARIANT 62
VARIANT 202
SEQUENCE 261 AA;

194 M 62 G 202 P 20385 MW;

MISSING (IN EARLY ELA 24 KI G -> E (IN STRAIN GRIDER). P -> G (IN STRAIN GRIDER). 4; P262C2BA CRC32;

KD PROTEIN)

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 257; Pred. No. 4.47e+00; 0; Mismatches 0; Indels Indels

0 Gaps

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178 LLCSLCY 184 ||||||| 862 LLCSLCY 868

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 1; Length 261; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

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30 DAVVIEQ 36 ||||||| 810 DAVVIEQ 816

ELL_DEC7 STANDARD: PRT: 261 AA.
P02125;

12.JUL-1956 (REL. 01, CREATE)
21.JUL-1966 (REL. 03, LAST SEQUENCE UPDATE)
21.JUL-1966 (REL. 03, LAST ASSOCIATION UPDATE)
01.ROV-1997 (REL. 33, LAST ASSOCIATION UPDATE)
01.ROV-1997 (REL. 33, LAST ASSOCIATION EPARE)
01.ROV-1997 (REL. 34, LAST ASSOCIATION EPARE)
01.ROV-1997 (REL. 35, LAST ASSOCIATION EPARE)
01.ROV-1997 (REL. 36, LAST ASSOCIATION EPARE)
01.ROV-1997 (REL. 36, LAST ASSOCIATION EPARE)
01.ROV-1997 (REL. 37, LAST ASSOCIATION EPAR VIRUSES; ADENOVIRIDAE; MASTADENOVIRUSES

PROTEIN)

SEQUENCE PROM N.A.
STRAIN-GOMEN;
MEDIJINE, B1237792.
MEDIJINE, B. DEXKER B.H.M., V
BOYER H. M.;
BOYER H. M.;
GENE 12:287-299(1980). Ş ORMONDT DE WAARD

TAKAHASHI E.,

EQUENCE FROM N.A. ENG H.X., HENTATI A., SIDDIQUE T.; ENBHITTED (FEB-1995) TO EMBH/GENBANK/DDBJ DATA BANKS

UPVI. NOMO BAPIENS (HUMAN). UMARTOVA: METAZOA: CRORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; UÇTHERIA: PRIMOTES.

SYMMETANT, MUTD. GLA-101.

BY MEDILINE, SQUISCA.

BY MEDILINE, SQUISCA.

BY MARKE Y. TAMAN. H., INGUE K., YOKOTA T., FUKUO Y.,

BY MARKE Y. TAMAN. H. TAMAN. H., INGUE K., YOKOTA T., FUKUO Y.,

BY MARKE Y. TAMAN. H. TAMAN. H., INGUE K., YOKOTA T., FUKUO Y.,

BY MARKE J. TAMAN. H. TAMAN. H. TAMAN. TAMAN. H. TAMAN. H. TAMAN. H. TAMAN. H. TAMAN.

CO 1. SUBMELITIAL ICANITON: CYTOPILASHIC.

CI SUBMELITIAL DEFECTS IN TIPL J. H. TIPL GAUSS OF ATAXIA HITH ISOLATED COUTTAINE DEFECTS IN TIPL J. H. AUTOSOMAL RECESSIVE DISEASE

CULTAMINE DEFECTS IN TIPL J. H. AUTOSOMAL RECESSIVE DISEASE

CO 1. SUMILARITY: TO CELULLAR RETINALDENTE BINDING PROTEIN.

SHILARITY: TO CELULLAR RETINALDENTE BINDING PROTEIN.

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MIH: 277460: -.
TRANSPORT: DISEASE MUTATION.
TRANSPORT: DISEASE MUTATION.
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CONFLICT 271 771 S -> R (IM REF. 2).
SEQUENCE 278 AA: 31749 MM; B3827397 CRC32;
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Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length Pred. No. 4.47e+00; 0; Mismatches 0; In 278; 0 Caps

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36 REAGVPL 42 ||||||| |230 REAGVPL 236

DESCRIT. 23 AA.

PAPAL STRUCC STANDARD; PRT; 278 AA.

PAPAL STRUCC STANDARD; PRT; 278 AA.

PAPAL STRUCTURES (REL. 32, CREATED)

TO 1.00V-1995 (REL. 32, LAST RECORRECE UPDATE)

TO 1.00V-1995 (REL. 32, LAST ANDVARION UPDATE)

TO 1.00V-1995 (REL. 32, LAST ANDVARION UPDATE)

TO 1.00V-1996 (REL. 32, LAST ANDVARION UPDATE)

TO 1.00V-1996 (REL. 32, LAST ANDVARION UPDATE)

STREPPUCCUCUS GORDONIC CHALLES

PROMANYOTA: FIRMICUTES; COCCLI STREPPUCCOCCAPAE.

DLINE: 95012638.
LENBRANDER P.E., ANDERSEN R.N., GANESHKUMAR N.;
PECT. IMMUN. 624469-4480(1994).

DIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE). ITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE

246 278 AA; 29705 MW: POTENTIAL
POTENTIAL
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232 GASVIGE 238 ||||||| 699 GASVIGE 705

TOJANOJSYMI STANDAND: PRT: 307 AA.
C PJ1097; 97 (REL. 35, CREATED)
T 01-80V-1997 (REL. 35, LAST ESDOENCE UPDATE)
T 01-80V-1997 (REL. 35, LAST ASMODATION UPDATE)
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SEQUENCE 307 9 110 GLY-RICH. AA; 34698 MW; 5E785CAD CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 307; Pred. No. 4.47e+00; 0; Mismatches 0; Indels 0 Caps

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129 VVSPARP 135 ||||||||| 294 VVSPARP 300

RESULT 25
ID SARB_SALTY STANDARD; PRT: 321 AA
C 956568;
DT 01_UN=1994 (REL. 29, CREATED)
DT 01_UN=1994 (REL. 29, LAST SEQUENCE UPDATE) 321 AA

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14.28_SCHPO STANDARD; PRT; 329 AA.
10930_SCHPO STANDARD; PRT; 329 AA.
10930_SCHPO STANDARD; PRT; 329 AA.
10.180V.1995 (REL. 32, LAST SEQUENCE UPDATE)
10.180V.1995 (REL. 32, LAST SEQUENCE UPDATE)
11.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
11.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
12.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
13.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
14.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
15.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
15.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
16.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
17.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
18.80V.1995 (REL. 31, LAST SEQUENCE UPDATE)
19.80V.1995 (REL. 31, LAST SEQUENCE UPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TD62_SCIPO STANDARD; PRT: 330 AA.

1010314;
01-007-1996 (REL. 34, CREATED)
01-007-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-007-1996 (REL. 35, LAST SEQUENCE UPDATE)
01-007-1999 (REL. 35, LAST ANNOTATION UPDATE)
01-007-1999 (REL. 35, LAST ANNOTATION UPDATE)
01-007-1990 (REL. 34, CREATED)
01-007-1990 (REL. 35, CREATED)
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250 ASRSLPL 256
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Q4753; P76839;
Q4753; P76839;
Q1-ROV-1997 (REL. 35, LAST SEQUENCE UPDATE)
Q1-ROV-1997 (REL. 35, LAST SEQUENCE UPDATE)
Q1-ROV-1997 (REL. 35, LAST ANDOMATION UPDATE)
DEPTIDE THANSPORTS TESTEM PERMENSES POTELIS
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SEQUENCE 329 AA; 36687 MM; 863653FB CRC32;
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PEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEMOLEME PROM N.A. VALSH S.V.;
STRAIN-972;
STRAIN-973;
SUBMITTED (JUL-1995) TO EMBL/CERNANK/DDBJ DATA BANKS.
-1- SIMILARITY STROND, TO YEAST YEROSSC.
BEBL: E5012; SUS2399; -
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Prokantota; gracilicutes; scotobacteria; pacultatively anaerobic rods;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALMONELLA TEPHINDRIIM.
BROKANYOTA: GRACILICUTES; SCOTOBACTERIA; PACULTATIVELY ANAEROBIC RODS;
SYTEROBACTERIACEAE.
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IMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
ROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC
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Pred. No. 4.47e+00;
O; Mismatches 0; Indels
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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-2 PROFEIN-DEPARTAL
-2 SUBPARITY
-2 SUBPARIT
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                      RESULT 30
ID EXOB_ACOBR STANDARD;
AC Q59083;
DT 01-NOV-1997 (REL. 35, CREATED)
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C P4705;
C P4705;
7 01-F28-1996 (REL. 3), CREATED)
7 01-F28-1996 (REL. 3), LAST SEQUENCE UPDATE)
7 01-007-1996 (REL. 3), LAST ANNOTATION UPDATE)
PETITO O ROTEIN.
N PETITO OR TAILOZIC OR J1282.
N PETITO OR TUNGI; ASCONTOCTIAN: PENIASCONTCETES.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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472 QLIRQHS 478
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786 STLTDLQ 792
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PORIL T.M., MALINOVIC G.

PORIL T.M., MALINOVIC G.

PORIL T.M., MALINOVIC G.

PORITION REFLIGENCE PETIDO NUTANTS ARE DEFICIENT IN MITOCHONDRIAL

PROPEZIM SYMPRESIS.

1- SUBCELLIAL LOCATION: MITOCHONDRIAL MATRIX (POTENTIAL).

ENGL; UJ7712: G1022819;

ENGL; 149398; G1060745;

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119 LAFGFAL 125
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-- SHILLARITY: WITH INTEGRAL MEMORANE COMPONENTS OF OTHER BINDING-

PROTEIN-DEPENDENT TRANSPORT STSTEMS. BELONGS TO THE OPPBC
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SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGORBOE FROM N.A.
STRAIN-KLI / PRAGS;
PESTEIN W., NOELEER E., STUNDE S., TEWES R., SCHMID R., BAKKER E.P.;
DANITYED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
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THALL STATE TO THE T. MANAGER T. MAN
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TRAIN-KLI / MC1655;
TALIWALE P.R. PLUNKETT G. III, MATHEM G.P., PERKA M.T., GLASHER P.D.;
PRITTED (JAN-1997) TO ENGL/GENDANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36063 MW;
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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Pred. No. 4.47e+00:
0: Mismatches 0: Indels 0:
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                                                                                                                                348 AA.
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I-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 1-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) 1-GLUCOSE 4-EPTHERASE (EC 5.1.3.2) (UDP-GALACTOSE 4-EPTHERASE) MIACTOWALDENASE).

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UESULT 31

DE PERZ_HOMAN STANDARU.)

TO PAILE 1995 (REL 31 CREATED)

TO 14NOV-1995 (REL 31 LAST SEQUENCE UPDATE)

TO 14NOV-1995 (REL 31 LAST SEQUENCE UPDATE)

TO 14NOV-1997 (REL 32 LAST SEQUENCE UPDATE)

DE PROSTACLANDIN EZ RECEPTOR. EPZ SUBTYPE (PROSTANDID EPZ RECEPTOR) (PGZ

RECEPTOR, EPZ SUBTYPE).

TOTERIA. --- (HUMAN). --- "ATTA: VERTEBRATA: TETRAPODA: MARGALIA:
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RESEQUENCE PROM. N.A.

RESEQUENCE PROM. N.A.

RESEQUENCE PROM. N.A.

RESEQUENCE PROM. N. RECERS V., VANDERLETDEN J.;

RE CERE 146.13-144(1994).

RE CERE 146.13-144(1994).

RE CORP. TAMILIERS V., VANDERLETDEN DEP-GALACTOSE.

CC -1- CANALYTIC ACTIVITI: UDP-GLUCOSE = UDP-GALACTOSE.

CC -1- MATERIAL ENCOLUTIONAL DE AND LIPOPOLIFEACCHARIDE BIOSYNTHETIC CC -1- PATERIAL T. WITH OTHER GALACTONALDENASES PROM. ETARRYOTIC AND CC -1- PATERIAL DE AUGUSTA DE CONTROLLEN D
                                                                                                                         REPORTE PROM N.

REPORTS P. GIERTA CA., KORN B., TASPO M.-L., POUTSKA A.,

RECURIES P. GIERTA CH. CREAU N.;

RA COSSET P. SINET P.-M., CREAU N.;

RE CERONICS 44:217-244(1997).

RECURRETER TENDANCY TO ALLOW POTASSIDM AS CHRACTERIED BY A

GENTER TENDANCY TO ALLOW POTASSIDM AS CHRACTED BY A

CONCEMPRATION OF EXTRACELLULAR POTASSIDM; AS EXTERNAL F: IS

CONCEMPRATION OF EXTRACELLULAR POTASSIDM; AS EXTERNAL F: IS

CONCEMPRATION OF EXTRACELLULAR POTASSIDM; AS EXTERNAL F: IS

CONCEMPRATION OF EXTRACELLULAR EXCUTIFICATION IS MAILE, DUE TO THE

CONCEMPRATION OF EXTRACELLULAR EXCUTIFICATION IS MAILE, DUE TO THE

CONCEMPRATION OF EXTRACE CONTENT IN INTERNAL MAGRESIM.

CONCEMPRATION OF THE INVADE RECTIFICATION IS MAILE, DUE TO THE

CONCEMPRATION OF THE INVADE RECTIFICATION IS MAILE.

CONCEMPRATION OF THE INVADE RECTIFIER TYPE R+ CHANNELS.

CONCEMPRATION OF THE INVADE RECTIFIER TYPE R+ CHANNELS.

CONCEMPRATION OF THE PROPERTY OF THE OF THE 
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|||||||
247 GGSASRS 253
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TISSUE-PLACENTA;
MEDLINE; 94359483.
REGAN J.W., BAILEY T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9941A; 099446; 000564;
11:807-1997 (REL. 35, LAST EXQUENCE UPDATE)
15-UL-1997 (REL. 35, LAST EXQUENCE UPDATE)
15-UL-1998 (REL. 36, LAST ANNOTATION UPDATE)
1479-SENSITYUZ INWARD RECTIFIER DOTASSIUM CHANNEL 15 (POTASSIUM
15ANNEL INWARD RECTIFIER POTASSIUM CHANNEL KIR 4.2) (KIRI.3)
KCN115 OR KCN114
KCN115 OR KCN114
KCN115 OR KCN116
KUNDON SAPTENS (HUDAN)
KUNTEROTA, METADON; CHORDATA; VERTEBRATA; TETRAPODA; MANGALIA;
KUNTERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
TISSUE-KIDNET:
EDLINE: 97150765.
HUCK H.E., PISER T.H., BOCK J.H., SLIGHTOM J.L., LEE
LENKOWSKI H.J.,
EDOL. CHEM. 272:586-593(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
ISSUE-KIDNEY:
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ASMID MEGADIASHID P90.
OKARYOTA: GRACILICUTES; SCOTOBACTERIA;
ROBIC, MOTILE, HELICAL AND/OR VIBRIOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRA M., SEKI N., NAGASE T., SUZUKI E., NOMURA N., OHARA O.,
TORI M., SAKARI Y., EKI T., MURAKAMI Y., SAITO T., ICHIKAWA
                                                                                               NNEL; ION TRANSPORT;
TRANSPORT.
            91
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            CYTOPLASMIC (POTENTIAL)
M1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    375
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C --- STUCKLIZIAN LOCATION: INTEGRAL MEMBRANE PROTEIN.

C --- STHICKTULAN LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECE

R MAIL: UN19487; G633550; ---
R MEMBL: UN19487; G633550; ---
R MEMBL: OCR_2009; ---
R MEMB
RP IDENTIFICATION OF PROBABLE FRAMESHIPTS.

RA CIBSON T.J.;

RI OMPOBLISHED OBSERVATIONS (MAR-1995).

CC --- CANALTIC ACTIVITY: ATP + D-GALACTOSE - ADP + D-GALACTOSE

CC --- PATRHAN: FIRST EXACTION OF GALACTOSE METABOLISM (LEIGH PATRHAY).

CC --- SANILARITY: TO OTHER PROAKANCYDIC AND EMARYOTIC GALACTONINASES.

C--- CAUTION: REF. 1 SEQUENCE DIFFESS FROM THAT SHOWN IN POSITIONS 49

CT TO 6.) 181 TO 244, AND 288 TO 310 DE TO FAMESHIPTS.

CC TO 6.5 181 TO 244, AND 288 TO 310 DE TO FAMESHIPTS.

CR PIR: C18663 KING.

C18663 KING.

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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CONFLICT
CONFLICT
SEQUENCE
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GALL STRLI STANDARD; PRT; 397 AA.
P3327?
01-JAN-1990 (REL. 13, CREATED)
01-NOV-1995 (REL. 12, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANOTATION UPDATE)
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TRANSMEM
DOMAIN
SITE
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|||||||
241 PGARRRG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
MEDILHE, 88086869.
ADMHS C.M., FORWHALD J.A., SCHMIDT P.J., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., FORWHALD J.A., SCHMIDT P.J., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., FORWHALD J.A., SCHMIDT P.J., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., SCHMIDT P.J., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., SCHMIDT P.J., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., ROSENBERG M., ROSENBERG M., BRAWMER M.E.;
ADMHS C.M., ROSENBERG M., ROS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREPTOMYCES LIVIDANS.
PROKARYOTA; PIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
235
245
375 AA;
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142
163
157
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245
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162
375
157
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HJ (POTENTIAL).

ROLE IN THE CONTROL OF POLYAMINE-MEDIATED CHARMEL GATING AND IN THE BLOKING BY INTRACELLIAR MAGNESIUM (BY SIMILARITY).

D > G (IN REP. 3).

V > A (IM REP. 3).

S - G (2M REP. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; Length 375;
Pred. No. 4.47e+00;
O; Mismatches 0; Indels
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Page 52

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Gaps

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RESULT
PROPERTY OF PROPERTY OF

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SUBSTITED (JAN-1995) TO ENGL/GERBANK/DEBS DAYA BANES.

-1 PRINCTION: RECEPTOR FOR PROSTACLANDE SZ (PEZ). THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY G-S PROTEINS THAT SYMMAPIS.

ADBRILATS CYCLASS: THE SUBSEQUENT BASES IN INTRACELLAR CAMP I
RESPONSIBLE FOR THE RELAXING EFFECT OF THIS RECEPTOR ON SHOOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DONELLO J.E., FAIRBAIRN C.E., KEDZIE K.M., WOODWARD D.F., GIL D.W.;
                                                                                                                                                                                                                                                                                                                                                    Score 7: DB 1: Length 358;
Pred. No. 4.47e+00;
O; Mismatches O; Indels
US-08-951-733-14.rsp
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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                                                                                                           OPAL_PSAKE STANDARD; PRT: 479 AA.
05.1397;
01.80v-1997 (REL. 35, CREATED)
01.80v-1997 (REL. 35, LAST ESQUENCE UPDATE)
01.80v-1997 (REL. 35, LAST ANNOTATION UPDATE)
01.80v-1997 (REL. 35, LAST ENGLENCE)
01.80v-1997 (REL 35, LAST ENGLENCE)
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671 KRAERLT 677
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P38845;
01-FEB-1995 (REL. 31, CREATED)
01-FCB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 31, LAST SEQUENCE UPDATE)
11-CCT-1996 (REL. 34, LAST ANUONATION UPDATE)
14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETIC 14-POTRETICAL 51.1 KD PROTEIN IN DCD1-MRPL6 INTERGENIC 14-POTRETIC 14-POTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PSOCAGE HAVE PANILY: 1. HER MANGRAME. HEROLYSIS TRANSPORT; FRANSFARE HAMBRAME. COMAIN 60 00 CYTOTANSHEM 60 80 POTENTIAL.

DOMAIN 60 40 POTENTIAL.

DOMAIN 61 470 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (2)

TOPOLOGY.

TOPOLOGY.

SCHULLEIN N., GENTSCHEV I., MOLLENKOPF H.-J., GOEBEL N.;

BULL GEN. GENTS. 314.155.433(1992).

FUNCTION: INVOLVED IN THE TRANSPORT OF HEMOLISIN A.

SUBCELLICLAN LOCATION: INEER MEMBANE-BOOKD (POTENTIAL).

THE TRANSPORT OF HEMOLISIN A.

FUNCTION: INVOLVED TO THE HIJD FAMILY OF SECRETION PROTEINS

DELL. HO133; LEECO.

PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: PROSITE: 
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1- SHILARITY: TO TEAST YNILT3C.
EMBL, U10397, G500655; -.
PJR, 546759; 546759.
RYPOTTETICAL PROTEIN.
SEQUENCE 465 AA: 51115 MH; 684873CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIJENCE PROM N.A.
SEQUENCE PROM N.A.
SEQUENCE PROM N.A.
SETALINE-1943FOOL

JOHNSTON H., ANDRESS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
DU E., FAVELLO A., FULTON L.; GATTUNG S., GEISEL C., KIRSTEN J.,
DU E., FAVELLO A., FULTON L.; GATTUNG S., GEISEL C., KIRSTEN J.,
KUCABA T., HILLIER L., JIER H., JOHNSTON L., LANGSTON Y.,
LARREILLE P., LOUIS B.J., MOCHI C., MADDIS E., LANGSTON R., MUSERE L.,
KHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAGGHAN K.,
VICANTI D., MILCOX L., WOELDMAN P., WATERSTON R., WILSON R.,
VICANTI D., MILCOX L., WOELDMAN P., WATERSTON R., WILSON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 PRRGAAP 383
|||||||
260 PRRGAAP 266
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     PSEUDOMONAS AERUGINOSA.
PROMARYOTA: GRACILICUTES: SCOTOBACTERIA: AEROBIC RODS AND COCCI:
PSEUDOMONADACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=396 / SEROTYPE 04;
WEDLINE; 85334404.
FELMLEE T. PELLETT S., WELCH R.A.;
J. BACTERIOL. 163:94-105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESCHERICHIA COLI.
PROMANYOTA, GRACIICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTENDANCTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-MAR-1999 (REL. 10, CREATED)
1-MAR-1999 (REL. 10, LAST SEQUENCE UPDATE)
1-CCT-1996 (REL. 34, LAST ANDOTATION UPDATE)
EMOLYSIN SECRETION PROTEIN D, CHROMOSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCHAROMYCES CEREVISIAE (BAKER'S YEAST).
KARYOTA; FUNGI; ASCONYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 CYTOPLASMIC (POTENTIAL).
80 POTENTIAL.
478 PERIPLASMIC (POTENTIAL).
54591 MW; 721A007E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7: DB 1: Length 397;
Pred. No. 4.47e+00;
O: Mismatches O: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGCHALTOTRIDLSGROLIPPDLAMEMELLIVVDTRYKHSIS

GGETGETGRAGCERGALLIGVML - EMGTPSGTSTYTEP

GGETGETSPRGCACWSGTFGASSTFARASTASARALAR

APROMASTR (IN REF. 1).

G >- ATFGASARSSBATFAARRIJFHLFPAGFGRRGGG

LECTR (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHQVAAVSRRERR -> PCRTRSRPSPGANDG (IN REF. 1).
RGGHALPLDTRDLSQRQIPPDLAAEGMRLLVVDTF
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                                                              RESULT 36
ID HLY4_ECOLI
AC P09986;
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MEDITE 2357011

MINISTER PLANTS PARTIEV I, MOLLEWROPF N.-J., GOZDEL W.;

MINISTER PLANTS PLANTS PARTIEV I, MOLLEWROPF N.-J., GOZDEL W.;

MOLL CEN. GENET, 241:55-163(1992)

CHOPPET PRINCIPS INVOLVED IN THE FRANSPORT OF HEDUTISH A.

CHOPPET PRODUCT PROTECTION: INNER HEMBRANE PROTEINS.

CHOPPET SIMILARITY BELONGS TO THE HUTD FAMILY OF SECRETION PROTEINS.

MINISTER PROSITE; BELONGS TO THE HUTD FAMILY OF SECRETION PROTEINS.

MINISTER PROSITE; MANSPORT; TRANSPORTANE; INNER HEMBRANE; PLASHID.

MINISTER PROSITE; PROSITE; MANSPORTANE; MINISTER HEMBRANE; PLASHID.

PT DOMAIN CONTROL OF THE PROTEINS PROTEINS.

SECRETION AND STATEMENT PROTEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative
Query Match
                                                        SECURNCE FROM N.A.
MEDILIES (5291165.
COMPELS U., MINSON A.A.
VINCLORY 133-3230-247(1986).
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
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-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL21.
-1- SIMILARITY: BELONGS TOGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 KRAERLT 218
|||||||
671 KRAERLT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 AAEHRLR 298
||||||||
553 AAEHRLR 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIAL POUR .

1. SERGELLIAN LOCATION: ATTACHED TO THE OUTER MEMBRANE BY A LIPID ANCHOR (PROBABLE).

1. STILLARIT: BELONGS TO THE FUSA/NOOT FAMILY.

ROKL: 97965; G199779; ...

PROSTITE: PROCHAID: ATTEMPORTER: L. LIPOPROTER: SIGNAL.

OUTER MEMBRANE; ANTIBIOTIC RESISTANCE; L. LIPOPROTEIN; SIGNAL.

SIGNAL.

20 479 OUTER MEMBRANE PROTEIN OPRJ.

LIPID 20 70 N-ACTE INCLUCIENTE (PROBABLE).

SEQUENCE 479 AA; 51873 MM; ASTECOAC CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIVD_ECOLI STANDARD: PRT: 478 AA.
P06779:
01-JAN-1988 (REL. 05, CREATED)
01-JAN-1988 (REL. 05, LAST SECONMICS UPDATE)
01-JAN-1988 (REL. 34, LAST ANNORMICS UPDATE)
01-OUT-1986 (REL. 34, LAST ANNORMICS UPDATE)
HENGLISH SECRETION PROTEIN D, PLASMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 AGPPSTS 126
|||||||
327 AGPPSTS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINSACHO, TSUJIMOTO H., EHAO Q., WADA A., TAMASAKI T.,
POOLE K., COTON N., TSUJIMOTO H., EHAO Q., WADA A., TAMASAKI T.,
HESHAT S., TAMASISHI J., NISHIMO T.;
SUBATITED (UUI-1958) TO SEBEL/CERBANK/DEBJ DATA BANKS.
SUBATITED (UUI-1958) TO SEBEL/CERBANK/DEBJ DATA BANKS.
SUBATITED (UUI-1958) TO SEBL/CERBANK/DEBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HEEM).
VIRIDAE: DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALDI.
ESCHERICHIA COLI.
PEASMID PHINIS2.
PROMANCOTA. GRACLICUTES: SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
SECUENCE FROM N.A.
SENS J., WELS W., VOGEL M., GOEBEL W.,
FENS MICROBIOL. LETT. 34:1-11(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09:28:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REL. 10, CREATED)
(REL. 10, LAST SEQUENCE UPDATE)
(REL. 24, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
0.7%; Score 7; DB 1; Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7: DB 1; Length 478;
Pred. No. 4.47e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
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US-08-951-733-14.rsp
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RESULT 39

ID UZ21_H9V11

AC P10205;

DT 01-MAR-1999 (1)

DT 01-DE-1992 (1)

DT 2591_1 101079;

DT 2591_1 10 STOCUENCE PROM N.A.

P STOCUENCE PROM N.A.

NECOLINE: 8879-327711912 M.A., DAVISON A.J., DOLAN A., PRAME M.C.,

NECOLINE: 8879-3271192 M. TANIDOR P.,

L. CER. VIENCE. 89-1331-2574(1988) TANIDOR P.,

CE. VIENCE. 89-1331-2574(1988) TO PARMILT TRATA GROUPS TOCETHER RSV-1 UL21,

CER. 101999: G22174(2).

DR EMBL. 201999: G22174(2).

DR EMBL. 201999: G221731;

DR PIR. C20084: PMSET1.

DR PIR. C20084: PMSET1.

DR PIR. C20084: PMSET1.

DR PIR. C20084: PMSET1.

DR PIR. C20084: PMSET1. 8 Best Local Similarity 100.0%; Natches 7; Conservative 137 LRVRAQD 143 ||||||| 717 LRVRAQD 723 RPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17). RIDAE; DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; (REL. 10, CREATED) (REL. 10, LAST SEQUENCE UPDATE) (REL. 24, LAST ANNOTATION UPDATE) STANDARD; Pred. No. 4.47e+00; 0; Mismatches 0; PRT; 535 AA Indels 0; ALPHAHERPESVIRINAE. Caps 0

용 Query Match 0.7%; Score 7; DB 1; Length 535; Best Local Similarity 100.0%; Pred. No. 4.47e-00; Matches 7; Conservative 0; Mismatches 0; Indels 137 LRVRAQD 143 ||||||| 717 LRVRAQD 723 Indels

0

Gaps

Ö

RESULT ID THE DIT OF THE TRAST STANDARD; PRT: 546 AA.

1112 TAST
112 TAST
113 CHEALTS; PRT: 546 AA.

114 TAST
114 TAST
115 CHEALTS; PRT: SEQUENCE UPDATE;
101 FER-1996 (REL. 18 LAST ANDOTATION UPDATE)
101 FER-1996 (REL. 18 LAST

Mon Dec 21 09:28:24 1996

Best Local Similarity 100.0%; Matches 7; Conservative O; Mismatches O; ö Caps 0

STE_METTH STANDARD; PRT; 552 AA.

959343;
01.NOV-1997 (REL. 15, CREATED)
01.NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOVATION UPDATE)
16-JUL-1998 (REL. 36, LAST ANNOVATION UPDATE) URS).

THANOBACTERIUM THERMOAUTOTROPHICUM (STRAIN MARBURG / DSM 2133). CIACEACTERIA; EURYARCHAEOTA; METHANOBACTERIALES;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 552; Pred. No. 4.47e+00; 0; Mismatches 0; Indels Indels 0 Caps

0

135 EDTDPRR 141 ||||||| 463 EDTDPRR 469

RESULT SY AC OZ STE_METH STANDARD; PRT; 553 AA.
078137;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
GLUTHATL-TRNA SYNTHETHASE (RC 6.1.1.17) (GLUTHANTE-TRNA LIGASE)

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Page

(GLORS), GENES). GLIX OB MISSI. METHANDANCIPEIUM THERMOAUTOTROPHICUM. ANCHAERACTERIA, EURYARCHAEOTA; METHANDBACTERIALES: METHANDBACTERIACEAE.

PEDUINCE PRON N.A.

9 SEQUENCE PRON N.A.

9 SEQUENCE PRON N.A.

10 C STRAIN-DEZIA H.

11 C STRAIN-DEZIA H.

12 C STRAIN-DEZIA H.

21 C STRAIN-DEZIA H.

22 C STRAIN-DEZIA H.

23 C STRAIN-DEZIA H.

24 SMITH D.R., DOUGETTE-STAMS L.A., DELOGGERY C., LEE H.-M., DUBOIS J.,

25 M. SMITH D.R., DOUGETTE-STAMS L.A., DELOGGERY C., GALBERT K.,

26 M. ALADROGE T. BASHERMADER R., BILANDER D., COOK R., GLIBERT K.,

27 MARIE R., CARUSO A., BUSH D., SAPER H., PAYMELL D., PRUBALAR S.,

28 MARIELS C.J., MOD J.-I., RICE P., MOLLING J., REPUE J.N.;

28 MARIELS C.J., MOD J.-I., RICE P., MOLLING J., REPUE J.N.;

29 MARIELS C.J., MOD J.-I., RICE P., MOLLING J., REPUE J.N.;

20 MARIELS C.J., MOD J.-I., RICE P., MOLLING J., REPUE J.N.;

21 DECENDANCE STATEMENT CONTINUE CONTI

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 553; Pred. No. 4.47e+00; O; Mismatches O; Indels

6 Gaps 0

136 EDTDPRR 142 ||||||| 463 EDTDPRR 469

RESULT TRACE OF TRACE TRAL_DACER STANDARD: PRT: 592 AA.
TRAL_DACER STANDARD: PRT: 592 AA.
1701.2BACPR STANDARD: PRT: 592 AA.
01.80V-1997 (REL. 35. LAST SEQUENCE OPDATE)
01.80V-1997 (REL. 35. LAST SEQUENCE OPDATE)
01.80V-1997 (REL. 35. LAST ANONANDO OPDATE)
TRAMSPOSASE FOR INSERTION SEQUENCE ELEMENT 1831.LIKE.
TREA. BACTEROIDES FRACILIS. PROMARYOTA: GRACILICUTES; SCOTOBACTERIA; AMAEROBIC RODS: BACTEROIDACELE.

SEQUENCE FROM N.A. STRAIN-RBF-103; MEDLINE; 94292468.

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EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES

SEQUENCE FROM N.A.
MEDLINE: 90375480.
AEBI M., KIRCHNER G., O
MARTIN N.C., ABELSON J CHEN J.Y.,

DIETRICH F.S. MULICAN J.T., HENNESSET K.M., ALLEM E., CHERT J.M.,
AVILES E., BERNA A., BERNAN T., CAREFFER J., CHEN E., CHERT J.M.,
CHUNG E., DURCAN M., GOENAN E., HARTZELL, G., SHUNICES-SHITH S.,
HYAME R., MAZER A., KOMP C., LASHMARI D., LEW H., LIN D.,
MOSERALE D., MAKAHAN K., RAMATH A., MORGREN R., DEFFER P., OH C.,
PETEL F.W., ROBERTS D., SELL P., SCHEMAM S., SENGLEN T., SHITH V.,
RATLOR P.M. MEI E., THOM M., BOTTETH D., DAVIS R.W.;
10MATITED (DEC-1594) TO ZBOMJ/ZERBAN/ZDDJ DAYA BANKS.

BY MINISTER MITTLE TON, AND SEQUENCE OF 19-26.

REMINISTER, THE STATISTICS, HOPERS A. K., MARTIN N.C.;

REMINISTER, C., LOUT Y.-C., HOPERS A. K., MARTIN N.C.;

REMINISTER, C., LOUT Y.-C., HOPERS A. K., MARTIN N.C.;

REMINISTER, C., LOUT Y.-C., HOPERS A. K., MARTIN N.C.;

REMINISTER, C., LOUT Y.-C., HOPERS A. K., MARTIN N.C.;

REMINISTER, MAD DOMATINE CARRIES OUT SETTEMENT STREAM CONTROL OF TERMINIST THE MINISTER PROPERTY OF THE MINISTER FRANCIST.

REMINISTER LOCATION: HITOCHOMBELL, MUCLEAR, AND CIPOPLASSIC.

REMINISTER LOCATION: HITOCHOMBELL, MUCLEAR, AND CIPOPLASSIC.

REMINISTER SETTEMENT: BELOGGE TO THE TRIA MUCLEOTIDITANSFERASE / POLY(A)

REMINISTER SETTEMENT: BELOGGE TO THE TRIA MUCLEOTIDITANSFERASE / POLY(A)

REMINISTER SETTEMENT SETTEMENT STREAM MUCLEOTIDITANSFERASE / POLY(A)

REMINISTER SETTEMENT SETTEMENT STREAM MUCLEOTIDIS SENA-BIDDING.

REMINISTER SETTEMENT SETTEMENT STREAM MUCLEOTIDE: NUMBER SETTEMENT.

REMINISTER SETTEMENT SETTEMENT STREAM MUCLEOTIDE: NUMBER SETTEMENT.

REMINISTER SETTEMENT SETTEMENT SETTEMENT.

REMINISTER SETTEMENT.

REMINISTER SETTEMENT SETTEMENT SETTEMENT SETTEMENT.

REMINISTER SETTEMENT
ALTERNATIVE : TRANSIT CHAIN INIT_MET INIT_MET 546 546 HINCOMOBION (POTEMILL).

TERN NUCLECTUDILITANSPERAGE,
HITOCHRODILLI.
POR CYTOPIASHIC/FULLAR PORM.
TERN NUCLECTIDILITANSPERASE, CYTOPIASHIC/
HUCLEAR CHOPIASHIC/FUCLEAR PORM.
TERN CUCLECTIDILITANSPERASE, CYTOPIASHIC/
HUCLEAR CUCLECTIDILITANSPERASE, CYTOPIASHIC/
HUCLEAR CUCLECTIDILITANSPERASE, CYTOPIASHIC/
HUCLEAR CUCLECTIDILITANSPERASE, CYTOPIASHIC/
HUCLEAR CUCLECTIDILITANSPERASE, CYTOPIASHIC/

Query Match SEQUENCE 546 AA; 62485 MW; 0.7%; Score 7; DB 1; 6ED4AD96 CRC32; Length

8

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\$220005E3

ROCES M. B. BENETT T. K., PANNE C.M., SMITH C.J.;
J. BLACTERION. 156.4366.4584(1994).
- PUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION EXPERIENCE FOR THE IS21/IS408/IS1163 FAMILY OF TRANSPOSIANE ELEMENT; DESCRIPT OF TRANSPOSIANE ELEMENT; TRANSPOSIANE ELE

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 1; Length 582; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

..

0

SALLALAMAN

331 LVARVLQ 337 ||||||| 102 LVARVLQ 108

SEQUENCE FROM N.A.
STRAIN=ISOLATE 1775;
MEDLINE, 94124015.
VERSALOVIC J., LUPSKI J.R.;
CENE 136:281-286(1993).

SENCIMENE PROM N.A.

SENCIMENE PROM N.A.

SENCIMENE D. ANDAS M.D., WHITE O., CLATTOM R.A., KLERNESS E.F.,

RELLANCED, A.M.D. ADMAS M.D., WHITE O., CLATTOM R.A., KLERNESS E.F.,

RELLANCE A. R., DULL C. J., DUDGE M. R., COCATE J. J. M.,

RELLANCE A. R., DULL C. J., FOLDE M. T., EELLAY C. A., COCATE J. J. M.,

RELLANCE A. R., DULL C. J., GLODE M. R., EELLAY C. M.,

RELLANCE C. R., LUNIA M.C., SENICOS T., REDEACH R. C. M.,

RELLANCE C. R., LUNIA H.C., PRIMAMA J. J., GRODER D. M., BRANDON R.C.,

RELLANCE C. M., RELLANCE M. R., C. M., SENICH M. R., SENICH M. R., C. M., SENICH M. R., SENICH

RESULT
AC PA

0

THE MARIN STANDARD: PRT: 593 AA.

OB3146:
01:MOV-1995 (REL. 31, CREATED)
10:MOV-1995 (REL. 32, LAST SEQUENCE OFDATE)
10:MOV-1995 (REL. 32, LAST SEQUENCE OFDATE)
10:MOV-1995 (REL. 32, LAST ASMOTATION OFDATE)
10:MARINGER US C 7.77.-7.
10:MARINGER US C 7.77.-7.
10:MARINGER US C 7.77.-7.
10:MARINGER US C 7.77.-7.
11:MARINGER US CONTROLLED U

RESULT 46

ID DOPO_MAT STANDARD: PRT: 620 AA.
AC 095'54.
AC 095'54.
DT 01-FEB-1995 (REL. 11, CREATED)
DT 01-FEB-1995 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 13, LAST SEQUENCE UPDATE)
DT 01-FOR-1997 (REL. 25, LAST ANNOTATION UPDATE)
DE PROPAMINE-META-NONCONTGENASE PROCUDEOR (EC 1.14.17.1) (DO DE PROCUTASE) (DBH).
GE MATTER NONCONTGENASE PROCUDEOR AT TETRAPODA: MAM
GE BEHAS NORWEGICUS (RAT).
GC EUTA-METONA, META-LOA, CHORDATA: VERTEBRATA: TETRAPODA: MAM
RN [1] HERIA; ROBENTIA.
RN SEQUENCE FROM N.A.
RX MEDILNE: 90119125.

(DOPAMINE

RESULT 47

ID ROC_SYNT3

AC P74177;
DT 01-NOV-1997 (I

(REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANDOTATION UPDATE)
D RNA POLYMERASE GAMMA CHAIN (EC 2.7.7.6).

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 1; Length 616; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

0

Gaps 0

105 LAPATPA 111 |||||||| 16 LAPATPA 22

WENTER 2.6.; 196-512(1995).

11 FUNCTION: INVOLVED IN PROTEIN EXPORT (BY SIMILARITY).

11 SUBJUT: 0.00E OF SEVEN SECRETORY PROTEINS (SECA-P 4 SECT) THAT

COURTISE THE PROLARYOIC PROTEIN TRANSLOCATION APPARATES

(BY SIMILARITY).

THE STATIAR LOCATION: INTEGRAL MEMBRANE PROTEIR. INNER MEMBRANE

KERLAWAGE A.R., BUIT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
MCHENBEY K., SUTTON G., PITEUGE M., PITEUGE J.D.,
SCOTT J.D., SHIRLEY R., LJU L.T., GLODEK A., KELLEY J.M.,
MEIDMAN J.F., PETILLIPS C.A., SPRIGGS T., HEDBLON E., COTTON H.D.,
TOTTERBACK T.R., HANN M.C., NGTYEN D.T., SAUDEK D.M., SHANDON R.C.,
FIRE D., FRITCHEAN J.L., PHENAMY J.L., GEOGRACH M.S. M.,
MEIDM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
WENTER J.C.,

-!- SUBCEL
-!- SINILA

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1998

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JAMON A., GERTMAN R., SABBAN E.L.;

J. ENTROSCI. RES. 25.35 -04(1990)

1. FUNDATION C. PROPARIZION OF DEPARTMET PRINCIPLE.

1. FUNDATION C. CONTINUE 3.4 -DININGAN PRINCIPLE AND MEMBRANE BOUND OF CONTINUE C.C.

1. FORDATION CONTINUE DEPTENDANCE PRINCIPLE AND MEMBRANE BOUND CC.

1. SORRANE C. ACCIVITY: 3.4 -DININGAN PRINCIPLE AND MEMBRANE BOUND CC.

1. SORRANE C. CONTINUE BILISTS AS BOTH A SOLUBLE AND MEMBRANE BOUND FORM ANY BE AND CC.

1. SORRANE C. CONTINUE BILISTS AS BOTH A SOLUBLE AND MEMBRANE BOUND FORM ANY BE AND CC.

1. SORRANE C. CONTINUE BILISTS AS BOTH A SOLUBLE AND MEMBRANE BOUND FORM ANY BE AND CC.

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D SECO_PARENN STANDAND; PRT; 616 AA.

C 944531; STANDAND; PRT; 616 AA.

C 144531; CREATED;

T 01-NOV-1995 (REL. 32, CREATED);

T 01-NOV-1995 (REL. 32, LAST SECONDEC UPDATE);

T 01-NOV-1995 (REL. 33, LAST SECONDATE);

T 01-NOV-1995 (REL. 32, LAST SECONDATE);

T 01-NOV-1995 (REL. 32, LAST SECONDATE);

T 01-NOV-1995 (REL. 32, LAST SECONDATE);

S 02-NOV-1995 (REL. 32, LAST SECONDATERIA; PACULTATIVELY ANA);

N 111-NOV-1995 (REL. 32, LAST SECONDATERIA; PACULTATIVELY ANA);

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Matches 7; Conservative
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231 EAGVPLG 237
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170 VLVHILA 176
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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CHRODOSOMAL DNA SYNTHESIZ.
CHRODOSOMAL DNA SYNTHESIZ.
OPP ZINC PER MOLECULE (BY SIMILARITY).
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Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7: DB 1: Length 692; Pred. No. 4.47e+00; 0; Mismatches 0; Indels

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Caps

0

46 SLEGALS 52 ||||||| 306 SLEGALS 312

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Page 66
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CCCCCT RESCOLA
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AC P3
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Matches 7; Conservative
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SECURING STOCKED S
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DOMAIN
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005000;
01F2D-1995 (REL. 31, CREATED)
01F2D-1995 (REL. 31, LAST SEQUENCE UPDATE)
15-UT-1995 (REL. 36, LAST ARROYNTION UPDATE)
15-UT-1996 (REL. 36, LAST ARROYNTION UPDATE)
00500ENTE CAMEL (FRANZENT).
00500ENTE CAMEL (FRANZENT).
LT 50
YKF4_YEAST STANDARD; F
P35732;
O1-JUN-1994 (REL. 29, CREATED)
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558 LREEILA 564
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1. CANALTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + RNA(N).

1. SUBUNITS: IN CYANOBACTERIA THE RNA POLYMENASE IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA, CAMPA, AND DELTA.

EMBL. D900131 (1653)543; CAMPA, AND DELTA.
                                                                                                     33 PPPAAPS 39
1111111
86 PPPAAPS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROOCI OR SIR1265. (STRAIN PCC 6803).
SINDEMOCYSTIS SP. (STRAIN PCC 6803).
PROKANYOYA, SEACILICUTES; OXYPHOYDBACTERIA;
CYANOBACTERIA (BLUZ-GREEN ALGAE); CHROOCOCCALES
CYANOBACTERIA (BLUZ-GREEN ALGAE);
                                                                                                                                                                                                                               551
568
605
662
671
705 AA;
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113
657
657
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568
605
670
706
74518 MW;
                                                                                                                                                                                                                               PHOSPHORILATION (BY CAPK AND
CAM-KINASE I).
PHOSPHORILATION (BY EAM-KINASE II).
PHOSPHORILATION (BY CAM-KINASE II).
PHOSPHORILATION (BY CAM-KINASE II).
NISOSLINA - KARPAJAPO (IN SYNAPSIN HE
MISOLICAN - KARPAJAPO (IN SYNAPSIN HE
MISOLICAN - CACAJ:
                                                                                                                                                                                                                                                                                                                                                                                  B (LINKER-DOMAIN).
C (ACTIN-BINDING AND STRAPTIC-VESICLE BINDING).
D (PRO-RICH).
E.
                                                                                                                                                                    Score 7: DB 1: Length 706:
Pred. No. 4.47e+00;
0: Mismatches 0: Indels
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Page 67

Page 68

RESULT 49

STANDARD; PRT; 706 AA.

ID SYNL_DOVIN STANDARD; PRT; 706 AA.

AC PATSES

DO 1-AGG-1990 (REL. 15, CREATED)

OL LAGG-1990 (REL. 35, LAST SEQUENCE UPDATE)

DO 1-AGG-1990 (REL. 35, LAST SEQUENCE UPDATE)

DO 15-THE 1996 (REL. 36, LAST ANNOTATION UPDATE)

DO 15-THE 1996 (REL. 36, LAST ANNOTATION UPDATE)

DO 2015 TAURIS (ROVINE)

CO 2015 TA

SECUENCE PROM N.A.
TISSUZE-BRAIN
TISSUZE-BRAIN
REDILHE, 0938255.
SIZEBOY T.C., CLEENIK A.J., KAO H.-T., TAKEI R., JOHNSTON P.A.,
SIZEBOY T.C., CLEENIK A.J., KAO H.-T., TAKEI R., JOHNSTON P.A.,
GEZEMAND P., CANAGIR S.D., WAGNER H.A., PERIN M.S., DE CAMILLI P.,
GEZEMAND P. (A) 1474-1480(1989).

X: RAY CRESTALLOCRAPHY (2.15 ANGSTROMS) OF 112-417.

MEDILER: 98130589.

BESER I., WANG C.B., HOSAKA H., SWAGULA C.S., SUDHOF T.C.,

DEIERMOPER J., WANG C.B., HOSAKA H., SWAGULA C.S., SUDHOF T.C.,

EMBO J. 17-971-984(1959).

BINDS TO THE CYTOSKELETON, AND IS BELIEVED TO FUNCTION IN THE

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COS SERVICE SE
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1 SILUMNES PROM N.A.
1 SILUMNES 10 1561-5661,394).
2 PARTICULUMNES 10 1561-5661,394).
3 PARTICULUMNES 10 1561-5661,394).
3 PARTICULUMNES 10 1561-5661,394.
3 PARTICULUMNES 10 1591-14.
4 PARTICULUMNES 10 1591-14.
5 PARTICULUMNES 10 159
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Best Local Similarity 100.0%;
Matches 7; Conservative
349 VAAPEEE 355
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457 VAAPEEE 463
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01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
REPOPHETICAL 84.0 KD PROFEIN IN NUPLIO-CSEM INTERGENIC REGION
TKLOS4C ON TKLOS.
SACCHAROFTCES CERVISIZE (BAKER'S TEAST).
EDIAROTAL FOREIX ASCONYCOTIAN; HEMIASCONYCETES.
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Pred. No. 4.47e+00;
0; Mismatches 0; Indels
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PRT; 738

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254 6 0.6 177 M CORPOTE STREAM SILE-NO CONTROL	Mon Dec 21 09:28:25 1998 US-08-951-733-14.rspt	152 6 0.6 6 6 5 044611 10005 9 PROTEIN 1513-00 1513-00 1515-00 16 6 6 6 9 10 10 10 10 10 10 10 10 10 10 10 10 10	Man Dec 21 09:28:25 1998 US-08-951-733-14.rspt .
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	Page 11		Page 9
\$100 6 0.6 382 14 09300 PDMA SINDING PROTEIN. \$110 6 0.6 383 1 005505 PDMATTCR INTERACTION. \$111 6 0.6 383 1 005505 PDMATTCR INTERACTION. \$112 6 0.6 384 1 005505 PDMATTCR INTERACTION. \$112 6 0.6 386 1 005505 PDMATTCR INTERACTION. \$113 6 0.6 386 1 005505 PDMATTCR INTERACTION. \$114 6 0.6 386 1 005505 PDMATTCR INTERACTION. \$115 6 0.6 401 1 00550	Mon Dec 21 09:28:25 1998 US-08-951-733-14.rapt	### Company of the Co	Mon Dec 21 09:28:25 1998 US-08-951-733-14-zept

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	Page 19		Page 17
917 6 0.6 1441 4 0.15074 KILLIDBIG RESISTANCE P 5.11e-02 918 6 0.6 1441 5 0.25074 KILANOSSE PROTEIN (PRAG STATE) 920 6 0.6 1441 5 0.25074 KILANOSSE PROTEIN (PRAG STATE) 921 6 0.6 1441 5 0.25074 KILANOSSE PROTEIN (PRAG STATE) 922 6 0.6 1441 6 0.25074 KILANOSSE PROTEINS (PRAG STATE) 923 6 0.6 1451 1 0.23489 KILANOSSE PROTEINS (PRAG STATE) 924 6 0.6 1554 4 0.14514 KILANOSSE PROTEINS (PRAG STATE) 925 6 0.6 1554 4 0.14514 KILANOSSE PROTEINS (PRAG STATE) 926 6 0.6 1554 4 0.14514 KILANOSSE PROTEINS (PRAG STATE) 927 6 0.6 1661 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 928 6 0.6 1661 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 929 6 0.6 1661 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 920 6 0.6 1661 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 921 6 0.6 1661 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 922 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 923 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 924 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 925 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 926 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 927 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 928 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 929 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 920 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 921 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 922 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 923 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 924 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 925 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 926 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 927 6 0.6 1764 1 0.00329 REPLICASE PROTEINS (PRAG STATE) 928 7 0.00329 REPLICASE PROTEINS (PRAG STATE) 929 7 0.00329 REPLICASE PROTEINS (PRAG STATE) 920 8 0.00329 REPLICASE PROTEINS (PRAG STATE) 920 8 0.00329 REPLICASE PROTEINS (PRAG STATE) 921 9 0.00329 REPLICASE PROTEINS (PRAG STATE) 922 9 0.00329 REPLICASE PROTEINS (PRAG STATE) 923 9 0.00329 REPLICASE PROTEINS (PRAG STATE) 924 9 0.00329 REP	Won Dec 21 09:28:25 1998 US-08-951-733-14.rept	### STATES SOCIETY PROPRETED NO. SOCIETY SOCIETY	Mon Dec 21 09:28:25 1998 US-08-951-733-14.zept

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Page 25
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Page 26
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RESULT 3

ID 035432 PRELIMINARY: PRT: 67 AA.
AC 035432 PRELIMINARY: PRT: 67 AA.
AC 035432 PRELIMINARY: PRT: 800 PRCE UPDATE)
DT 01-JAN-1998 (TREMBLEEL. 05, LAST SHOURCE UPDATE)
DT 101-GO-1998 (TREMBLEEL. 07, LAST SHOURCE UPDATE)
DE TELOMERASE CATALUTIC SUBUNIT (FRANCENT).
OS HUS MUSCULUS (MOUSE).
OC EUTHARYOTA, METALDA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA:
OR EUTHARYOTA, METALDA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA:
OR EUTHATE, COLFTEANU J.L.;
R. SOURCE FROM N.A.
AR SSSIR (CLETEANU J.L.;
R. BANGER (T. SOURCE)
DR BEBLETTE (T. SOURCE)
DR BEBLETTE (T. SOURCE)
THE MOULTR (T. GT 67

FT NOW_TER (T. GT 67)

SOURCE (F AA): 8368 MW; EZAOSFDB CRC37;
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10 070312 PRELIMINARY; PRT; 1122 AA.
10 070312, CREMINED: 07 CREMINED: 07 01-ANG-1998 (TREMILER: 07 CREMINED: 07 01-ANG-1998 (TREMILER: 07 LAST ENQUENCE UPDATE)
DT 01-ANG-1998 (TREMILER: 07 LAST ENQUENCE
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Best Local Similarity 100.0%; Pred. No. 6.15e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
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opery Match 0.9%; Score 9; DB 4; Length 632;
Best Local Similarity 100.0%; Pred. No. 6.15e-04;
Matches 9; Conservative 0; Mismatches 0; Indels
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SEQUENCE FROM N.A.
SEQUENCE R., CLEFFELAND J.L.;
SUBMITTED (CCT.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (CCT.1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
BEBGL: APO29215; G2605903;
NOW_TER 67 67
SEQUENCE 67 AA; 8368 MM; E2A06F2B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             - 104403 PRELIMINARY; PRT; 632 AA.
014497: (PERGILEEL 05, CREATE)
01.JNN-1988 (PERGILEEL 05, LAST GROUNDE UPDATE)
01.JNN-1988 (PERGILEEL 06, LAST ANDOTATION UPDATE)
10.JNN-1988 (PERGILEEL 06, LAST ANDOTATION UPDATE)
10.JNN-1988 (UDAN)
1000 SETEMS (UDAN)
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119 LAFGFALLD 127
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HEDLINE: 873098).

HEDLINE: 873098).

PROC. NATL. ACAD. SCI. U.S.A. 84.5354-5358(1987).

PROC. NATL. ACAD. SCI. U.S.A. 84.5354-5358(1987).

SIGNAL HATSON SERVICE POPERTIAL.

1 23 2183 U.S. GLICOROTEIN.
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                                                                                                                   SEQUENCE FROM N.A.
HEDLINE: 9737002
YOKODCHI M., SUEUXI R., MASUHARA M., KOMIYA S., INOUE
YOKODCHI M., SUEUXI R., MASUHARA M., KOMIYA S., INOUE
YOKODCHI M., SUEUXI R., MASUHARA M., KOMIYA S., INOUE
ZOMICA MADOODED 15715(1997)
PEMA: PEPOMOTY SHI.
PEMA: PEOMOTY SHI.
SEQUENCE 633 AA: 67727 MM; AB4DBOBD CRC33;
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NOW TER 183 183
SEQUENCE 183 AA; 18601 MW; 37DE42ED CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (PREMIJERI, 01, CERATE)
01-NOV-1996 (PREMIJERI, 01, LAST ANNOTATION UPDATE)
01-NOV-1996 (PREMIJERI, 01, LAST ANNOTATION UPDATE)
14-5 GILCODROTELL PRECURSON (FRAGMENT).
WIS MISCULDS (MOUSE)
FULLANTOTA, METALON, CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA;
DUTHERIA; ROBENTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       841 LCSICYGDMENKLFAGIRROGILLBLYDDPILYTPHLTHAKTFLATLYRGYPETGCYVNL 900
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DESCRIPTION

OCIDIO,

AC GORDIS,

PRELIMINARY,

PRT: 24 AA.

AC GORDIS,

PT 01-807-1996 (TREMELET, 01 CREATED)

DT 01-807-1996 (TREMELET, 01 LAST ENGUENCE UPDATE)

DT 01-807-1996 (TREMELET, 01 LAST ANDOTATION UPDATE)

DE TRANSHEMENTE GLYCOPROTEIN (FRACHENT).

ON LY-5,

GN LY-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD
M
RESULT 9

ID 01339 PRELIMINARY; PRT: 989 AA.

C 01339; (TREMBLEEL 05, CREATED)

DT 01-JAN-1998 (TREMBLEEL 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLEEL 05, LAST ANDVANTION UPDATE)

DT 01-JAN-1998 (TREMBLEEL 05, LAST ANDVANTION UPDATE)

TELOMERASE REVERSE TRANSCRIPTASE 1.
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.0%;
Matches 9; Conservative
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Best Local Similarity 100.01; Pred. No. 2.62e 42;
Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LAFGFALLD 18
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119 LAFGFALLD 127
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ENGL; AFOSI911; G3005592: --
RNA-DIRECTED NAN POLIFERISE.
SEQUENCE 1122 AA; 127977 MM; 222075D6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENUMBER FROM N.A. BARBELL B.G., VOICHAERT G.;
ETRALINSTEIN, BAINDREAM A., BARBELL B.G., VOICHAERT G.;
EURHITTED (MA-1598) TO ENEL/GENDANK, DEBJ DATA BANKS.
ENGL; MOLSTB3; CISTAGOS;
ENGL; MADISTB3; ELSESSOS;
ENGL; MADISTB3; ELSESSOS;
ENGL; MADISTB3; ELSESSOS;
ENGL MADISTB3; ELSESSOS;
ENGL MADISTB3; ELSESSOS;
ENGL MADISTB3; ELSESSOS;
ENGL MADISTB3; ELSESSOS;
ENGLESSES BE AA; 116538 MW; 39C385A7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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MEDLIER: 9906862.
SACA T. TURA J.S., SHEM P.W.W., PANCOAST T.C., BOYSE E.A.;
MACL. SELL. BLOL. 8:4889-4895[1980].
EMBL. MAJSA: 0554192; .
EMBL. MAJSA: 0554192; .
MALTERNATIVE SPLICING: TRANSMEMBRANE.
MON.TER 34 24
SEQUENCE 24 AA: 2717 MW: 7A10DDDA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JOG-1998 (TREMBLREL. 07, LAST ANYOTATION UPDATE)
TELMERASE REVERSE TRANSCRIPTASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUS MISCULIS (MOUSE).
EURANYOTA, HETALOA; CHORDATA; VERTEBRATA; TETRAPODA; HAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUTHERIA; RODENTIA.
[1]
                                                                                                                                                                                                                                                                                                                                                                703 GIPQGSILS 711
|||||||||
852 GIPQGSILS 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STOURNCE FROM N.A.
STRAINS-973H.;
MEDINE; 9740633 G.B., CHAPMAN K.B., WEINRICH S.L., ANDREWS W.H.,
MARAGER J. M.LECT C.B., CECH T.R.;
SCIENCE J. 71:955-959(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 VRAQDPPPE 523
||||||||
719 VRAQDPPPE 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHIZOSACCHARONTCES POMBE (FISSION TEAST).
SURARYOTA; FUNGI; ASCONYCOTINA; HEMIASCONYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09:28:25 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 9; DB 3; Length 988;
Pred. No. 6.15e-04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9: DB 11; Length 24;
Pred. No. 6.15e-04;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        988 AA
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SCHIZOSACCHAROMYCES POMBE (PISSION TEAST). EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES

HOD

STAINS-973H: STAINS-973H: SENDERS PROM N.A.
STAINS-973H: STAINS-973H:

ANDREWS W.H.

8 8

704 GIPQGSILS 712 ||||||||| 852 GIPQGSILS 860

Overy Match 0.9%; Score 9; DB 3; Length 989; Best Local Similarity 100 Ob; Pared. No. 6.15e-04; Matches 9; Conservative 0; Himmatches 0; Indels

6

Caps

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Caps
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RESULA: 111

DE SULA: 121

DE SULA: 121

DE SULA: 121

DE SULA: 122

DE SULA: 122

DE SULA: 123

DE 8 LAPGFALLD 16 |||||||| 119 LAFGFALLD 127 9; Conservative 0 Mismatches 0 Indels HAMMALIA; 0

RESULT 1
10 061081
AC 0610 Query Match 0.9%; Score 9; Best Local Similarity 100.0%; Pred. No. SEQUENCE 23 24 1291 1291 AA; 1445 23 POTENTIAL. 191 LYMPHOCYTE COMMON ANTIGEN 144559 MW; 63481A8D CRC32; DB 11; Length 1291; 6.15e-04;

JUZ 10

GENERAL DE PREZIMINARI;
GENERAL DE CERRATED)
GENERAL DE CHEMINARI;
GENERAL DE CHEMINARI;
GENERAL DE CHEMINARI,
GENERAL GENERAL GENERAL GENERAL TETRAPODA; MAMMALIA;
GENERAL RODENTIA.
GENERAL RODENTIA.
GENERAL RODENTIA.
GENERAL GENERAL

SECURNE FROM M. T.
ZERDZES L. BARRIT D.S., RASCHEZ W.C.;
DPY. COMP. IMMUNCL 1; 243-254(1991).
ZEGL. M9231 G.1980.7;
MCD. MCI. S7310 G.1980.7;
PROSITE. PSO0131 TR. PHOSPHATASE_1; 2.
PRAN. PPO0103; T.Dhosphatase.
STANL PRO1013.5.
STANL PRO1013.5.

Ouery Match 0.9%; Score 9: DB 11: Length 1343: Best Local Similarity 100.0%; Pred. No. 6.15e-04: Matches 9: Conservative 0: Mismatches 0: Indels EMBL. M31151 C187402 JOINED
EMBL. M31151 C387402 JOINED
EMBL. M31154 C387402 JOINED
EMBL. M31155 C387402 JOINED
EMBL. M31156 C387402 JOINED
EMBL. M31156 C387402 JOINED
EMBL. M31156 C387402 JOINED
EMBL. M3156 C3 1343 1343 1343 AA; 150679 MW; 984DFAEB CRC32; Length 1343; ö Gaps 0

DESCRIPTION

TO 065310

DO 701-NOV-1996 (TREMBLEEL. 01.48

DO 101-NOV-1996 (TREMBLEEL. 01.48

DO 101-NOV-1996 (TREMBLEEL. 07.48

DO 101-NOV-1996 (TREMBLEEL. CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) PRT; 146 AA

PRICAN SWINE FEVER VIRUS (ASFV)

YUSTE L., ENRIQUEZ

SEQUENCE FROM N.A.
STRAIN-BA71V:
CA VEGA I., GONZALEZ A., BIASCO
VIROLOGY 201:152-156(1994). R., CALVO V.,

VINUELA E.

ð 8 8 LAPGPALLD 16 |||||||| 119 LAPGPALLD 127

IRIDOVIRIDAE

EQUERCE FROM N.A.
TRAIN-BA'IV;
NAEZ R.J., RODRIGUEZ J.M., NOGAL M.L.,
DDRIGUEZ J.F., VINUELA E.;
IROLGOY 108-249-278(1995).

SEQUENCE PROM N.A.
STRAIN-BATVY

KEDLINE: 90219205.
GONALES A. CALVO V. ALMARAN F., ALMENDRAL J.M.,
LA VERA I., BLASCO R., VINELA E.)
J. VIROL. 64:2073-2081(1990).
[4]

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SEQUENCE FROM N.A. STRAINBATIV; HEDLINE; 90219204. ALMENDRAL J.M., ALMAZAN F., BI ALMENDRAL J.M., ALMAZAN F., BI J. VIROL. 64:2064-2072(1990). BLASCO R., VINUELA E.;

SEQUENCE FROM N.A.
STRAINERATIV:
MEDINE: 91134988.
CAMACHO A., VINUELA E.;
CAMACHO TEL:251-257(1991).

BEQUENCE FROM N.A. STRAIN-BA71V; LLMAZAN F., MURGUIA J.R., J., GEN. VIROL. 0:0-0(0). RODRIGUEZ J.M., 5 VEGA

VINUELA

SEQUENCE FROM N.A.
STRAIN=BA71V;
MEDLINE; 94187118.
RODRIGUEZ J.H., YANEZ R.J.,
VINUELA E.; PAN R.,

VIROL. 68:2746-2751(1994).

SEPOTENCE FROM N.A.
SEPOTENCE FROM N.A.
SEPOTENCE PROBLEME J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., RODRIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., RODRIGGER J.P., SALAS M.L., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., PORTIGGER J.H., VINGELA E.,
YAMEE R.J., PORTIGGER J.H., VINGELA E.,
YAMEE R.J., VINGELA E.,
YAMEE

SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINS-94056556
MEDLINE: 94056556
ALCAMI A., ANGULO A., VINUELA E.:
J., GEN. VIROL. 74:2317-2324(1993).

SEQÜENCE FROM N.A.
STRAINEBAIV.
MEDLINE; 93277388.
MINOZ M., FREIJE J M., SALAS M.L.,
MINOZ M., FREIJE J M., SALAS M.L.,
ARCH. VIROL. 130:93-107(1993). VINUELA

SEQUENCE FROM N.A.
STRAINS-BAJIY.
STRAINS-BAJIY.
MEDIJNE: 90337780.
MEDIJNE: 90337780.
MEDIJNE: 90537780.
VLYUDEJA E.
VLYUDEJA E.
VLYUDEJA E.
1121-304(1990). MUNOZ M., BOCKAMP E.O., SIMON-MATEO

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Best Local Similarity 100.0%; Pred. No. 1.03e-01;
Matches 8; Conservative 0; Minnatches 0; Indels
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Best Local Similarity 100.0%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9017 13
9017 13
9018 PRELIXINARY:
905547 996 (PREMINERE. 0), C:
01-80V-1996 (PREMINERE. 0), C:
01-80V-1996 (PREMINERE. 0), L:
01-80V-1996 (PREMINERE. 0), L:
01-80V-1996 (PREMINERE. 0), L:
01-80V-1996 (PREMINERE. 0), L:
01-80V-1996 (PREMINERE. 1-1), L:
01-80V-1996 
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|||||||
142 RSYLPHTV 149
                                                                                                                                                                                                                                   083745; PRELIMINAN: PRT: 342 AA.
083745; OL-NOV-1996 (TREMGLEEL. OL. CREATED)
01-NOV-1996 (TREMGLEEL. OL. LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMGLEEL. OL. GAST ANNOTATION UPDATE)
01-NOV-1996 (TREMGLEEL. OL. LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMGLEEL. OL. CREATED)
0
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||||||||
| 243 ARRRGGSA 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 09:28:25 1998
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STRAINSBAILY.
MEDIZNE; 94133986
RODRIGUEL J.H., YANEE R.J., F
GENE 136:103-110(1993).
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STRAIN-COOPERS
KHAUR A., TIXOO S.K., BABIUX L.A., HURK S.;
GENE 0.0-0(0).
SENDURNCE 318 AA. 35930 MF; 4F818424 CRC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEDLIKE; 9381190.
TANEZ R.J. BOGRSNEL M., NOGAL M.L., YUSTE L., VINUELA E.;
NUCLEIC ACIDS RES. 21:2423-2427(1993).
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STRAIN-BAILY.
MEDLINE: 93377788.
SIMON-MATEO C., ANDRES G., VINUELA E.:
EMBO J. 12:2977-2987(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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TRAINHEANIY.
CEDLINE: 9353606.
CODRIGUEZ JM., YANEZ R.J., ALMAZAN F.,
YIROL. 67:5312-5320(1993).
EQUENCE FROM N.A.
EDILINE: 84216451.
TACEY A., ARBUTHNOTT C., KOLLEK R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDLINE: 93233210.

RADOS P.J., VINUELA E., ALCAMI A.;
VIROL. 67:2475-2485(1993).
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                            DODENCE FROM N.A.
TRAINHBATUY
EDLINE: 9023993
ODEE-OTIN C., FREIJE J.M., PARRA F.,
IROLOGT 175:477-884(1990).
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PEALN-BAJU:
PEALN-BAJU:
PELNE: 9226660 . LOPEE-OTIN C.,
RENACOSA A. L. VINDEA E.;
VIROL. 66:3860-3868(1992).
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NEE R.J., RODRIGUEZ J.M.,
NE 134:161-174(1993).
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338 AA: 35930 NW; 4F818424 CRC32;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.03e-01;
0; Mismatches 0;
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                 COGGINS L., OSTERTAG W.;
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                                                                                          MENDEZ E., VINUELA E.;
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RECULT 15

RECULT 191

RECULTION TO CAPACITY (TREBLEEL, 04, CREATED)

DT 01-UUL-1997 (TREBLEEL, 04, LAST SEQUENCE UPDATE)

DT 01-UUL-1997 (TREBLEEL, 05, LAST SHORDATION UPDATE)

DE CHARTON, RETALOA: CROTADATA: VERTEBRATA: TETRAPODA: AVES: NEOCHATHAE:

RECULTER SHOULE FROM N.A.

RET 115SUEVANDERM (LANN)

RE ULTE: 191088 (LANN
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ID 015740
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Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local Similarity 100.0%;
Matches 8; Conservative
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STRAIN-BA71V;
NEDLINE; 92007485,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SENTENCE FROM N.A.
STRAINSANIY.
MIDCHINE; 92463907.
MIDCHINE; 92463907.
FREIJE J.H., I
SALANS H.L.;
SALANS H.L.;
CARCINGY 188:938-947(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRANTH-BA71V;
MEDLINE: 95159428.
SIMON-MATED C., FREIJE J.H., A
VIROLOGY 206:1140-1144(1995).
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MEDLINE: 9700876.

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MEDLINE: 15::11-727(1997).

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MEDLINE: 15::10-727(1997).

MEDLINE: 1
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EMGL. KO1683: G337293: -
EMGL. KO1683: G337293: -
PROSTITE: PSO1016: PACTERIK_LIMAGE_ST: 1.
PSPAH: PRO10059: PALIAMSE.
COAT PROTEIN: EMPTLADPE PROTEIN:
SEQUENCE 342 AA: 37871 MM: 90F93921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEOCUENCE FROM N.A.
STRAIN-BARTY,
TANDE R.T. (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; Uls465; G-190518; ·.
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STRAINEBAJYY
MEDILHE: 97016328
GONRALEE A., TRAAVERA A., ALZENDRAL J.M., VINUELA E.;
NOCLEIC ACIES RES. 14:6835-6844(1986).
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GENALMENTINE
HEDLINE: 94091055.
TREALTE J.M., LARIN G., VINUELA E., LOPEZ-OTIN C.;
YINGE RES. JOSS-72(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIROLOGY 193:531-536(1993).
                                                                                                                                                                                                                                            128 PYGVLLKT 135
|||||||
426 PYGVLLKT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 LRPSLTGA 298
||||||||
372 LRPSLTGA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEQUENCE FROM N.A.
TEXALINDATU:
STRAINDATU:
STRAINDATU
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STRAINHANIY.
PERAL I., TANES R.J., REVILLA Y., VINUELA B., SALAS M.L.;
VIROLOGI 19::11-38(199).
                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8; DB 14; Ler
Pred. No. 1.03e-01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8: DB 13: Length 508:
Pred. No. 1.03e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VINUELA E.;
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                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOPEZ-OTIN C., BLASCO R., VINUELA
                 680
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STREETHOOGSERTTTA

166 REEILAKF 173 |||||||| 559 REEILAKF 566

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RESULT DD

RESULT DD

RESULT DATA

AC 065932; PRELIMINARY; PRT: 37 AA.

AC 065932; PRELIMINARY; PRT: 37 AA.

AC 065932; PROTESTATED;

DT 01.AGC-1998 (TREMBLEEL O7, LAST SECRETE UPDATE)

DT 01.AGC-1998 (TREMBLEEL O7, LAST SECRETE UPDATE)

DT 01.AGC-1998 (TREMBLEEL O7, LAST SECRETE UPDATE)

DE HYPOTIETICAL 4.2 XD PROTEIN (FRANCHENT)

OS LICOPERSICON ECCLENTUM (TOWAND).

CE SULANTA: BEBRYOPHYTA: ANGIOSPERMAE: DICOTYLEDONEAE:

RM (1)

RM SECRETE STANKEELS S. ARGELLIS A. R.:

RM AGELIS A. RAELLIS A. R.:

RM HYPEL: AGORGES ET18450S;

TH WINDLES HOOSESS ET18450S;

TH WOMEN BOTTES

TH NOTES 37 AA: 4205 MM; SC7621EO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 17

ID 024144 PRELIMINARY: PRT: 869 A.
AC 024144 PRELIMINARY: PRT: 869 A.
DT 01-NOV-1996 (TREMELREL. 01 CREATED)
DT 01-NOV-1996 (TREMELREL. 01 LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMELREL. 05, LAST ANNOTATION UPDATE)
DE INTURNED PROTEIN.
OS DROSOPHILA MELANGASTER (PRUIT FLY)
OS DROSOPHILA MELANGASTER (PRUIT FLY)
CE ZULANTOTA: METANOA. ARTHROPODA: INSECTA: DIFTERA.
HE 11 LUTCHE PROM N.A.
RE MEDITARE PROM N.A.
RE PLEMER: PSHONOLUSS: INAP E.J., ADLER P.N.:
RESUL USTITAL GLISSOFIT.
DR PETANER: PSHONOLUSS: INAP E.J., ADLER P.N.:
RESUL USTITAL GLISSOFIT.
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Best Local Similarity 100.0%; Pred No. 1.03e-01;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query March 0.8%; Score 8; DB 5; Length 680; Best Local Similarity 100.0%; Pred: No. 1.03e-01; Marches 8; Conservative 0; Mismatches 0; Indels
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STRAIN-NAI, OFFICE FROM N.A.
STRAIN-NAI, OFFICE FROM N.A.
STRAIN-NAI, OFFICE FROM N.A.
STRAIN-NAI, OFFICE FROM N.A.
SUBMITTED (MOG-1597) TO EMBL/GENBANK/DEBJ DATA BANKS
SUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          015740;
01-JAN-1998 (TREMGLERI. 05, CREATED)
01-JAN-1998 (TREMGLERI. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMGLERI. 05, LAST ANNOTATION UPDATE)
PKSA (FRACHENT).
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STRAIN-04-2;
STRAIN-04-2;
MEDILIE: 96059477.
MADIZDOL L. GALTIER M.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADIZDOL L. GALTIER M.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADIZDOL L. GALTIER M.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADIZ, CITYLO; G881410; -.
MARIX, PROTZIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DICTYGGTELIUM DISCOIDEUM (SLIME MOLD)
EURARYCTA; PROTUZOA; SARCOMASTIGOPHORA; SARCODINA; RHIZOPODA;
EUNYCETOZOA; DICTYGGTELIA.
                                                                                                                                                                                                                                                                                      Score 7; DB 10; Length 37;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 5; Length 23;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB72C0F4 CRC32;
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                                                                                                                                                                                                                                                                                            Gaps
Bd
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                                                                                                                                                 RESULT 22

IREG 05380

PRELIMINARY, PRT; 109 AA.
AC 05380,
DT 01-309/1996 (FREMELREL 01, CREATED)
DT 01-309/1996 (FREMELREL 01, LAST SECREMCE UPDATE)
DT 01-309/1996 (FREMELREL 01, LAST SECREMCE UPDATE)
DE HEPA (FRAMENT).
DE HEPA (FRAMENT).
OF PLASHID PECANO2.
OC PROMATOTA, BACTERIA, FIRMICUTES; GRAM-POSITIVE COCCI,
OC STREPPOCOCCICCEME.
RN [1]
RP SECUENCE FROM N. A.
EC STRAIN-CCSA;
DATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 19
ID 027174;
PRELIMINARY; PRT: 23 AA.
AC 027174;
DT 01-NOV-1996 (TREMBLEEL 01, CREATED)
DT 01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
DT TRICHOCTS MATRIX PROFIELT 12 (FRAGMENT).
DE TRICHOCTS MATRIX PROFIELT 12 (FRAGMENT).
RY SEQUENCE PROM N.
RY SEQUENCE PROM N.
RY SEQUENCE PROM N.
RY SECUENTE 15: 329-335(1894).
RN EDCCHMET 56: 329-335(1894).
RN [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID 060300 PRELIMINARY;
AC 060300; PREMIMEL. 07, C
D7 01-NG-1998 (TREMBLEEL. 07, L
D7 01-NG-1998 (TREMBLEEL. 07, L
D7 01-NG-1998 (TREMBLEEL. 07, L
D8 KLAN0553 PROTEIN (PRACHENT).
C8 MICHANOSSI PROTEIN (PRACHENT).
C8 MICHANOSSI PROTEIN (PRACHENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dec 21 09:28:25 1998
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 8; Conservative
Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LVAPSCA 58
|||||||
183 LVAPSCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               941 ALAPATPA 948
|||||||
15 ALAPATPA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          052175 PRELIMINARY: PRT: 87 AA.
052175-1998 (TREMBLEL 05, CREATE)
01-VDN-1998 (TREMBLEL 05, LAST SEQUENCE UPDATE)
01-VDN-1998 (TREMBLEL 07, LAST ANNOTATION UPDATE)
PLASHID PRET: COMPLETE PLASHID SEQUENCE.
87AMONELLA BERTA.
PLASHID PRET: GRACILICUTES: SCOTOBACTERIA: PAGULTATIVELY ANAEROBIC RODS:
BYTHOROGOGY GRACILICUTES: SCOTOBACTERIA: PAGULTATIVELY ANAEROBIC RODS:
BYTHOROGOGY GRACILICUTES: SCOTOBACTERIA: PAGULTATIVELY ANAEROBIC RODS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-BRAIN: TSHIKAWA K., MITAJIWA N., TANAKA A., I
MAGASE T., ISHIKAWA K., MITAJIWA N., TANAKA A., I
ORARA O., I
DAN RES. 5:11-39(1998).
DAN RES. 5:11-39(1998).
TEMPL, ABOLILIZS, D1026609; -.
NOW_TER
1004_TER
1095_AA: 118835_M9; 43474254_CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLASMID.
SEQUENCE 87 AA; 9613 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE PROM N.A.
STRAIN-04-2;
MEDIJNE; 9513139
MEDIJNE; 9513139
MADERDO L., GAUTIER M.C., LE CAER J.P., DE LOUBRESSE N., SPERLING L.;
BIOCHIEZ 16-232-335(1994)
                                                                                                                              NON_TER 1 1
SEQUENCE 109 AA; 11728 MW; DODF954B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPÓUENCE FROM N.A.
BIANES D.E., KEASLER S.P., LAMPEL K.A.;
SUBHITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
BUBL: AF025795; G2689636; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARAMECIUM TETRAURELIA.
SUKARYOTA; PROTOZOA; CILIOPHORA; CILIATA; HOLOTRICHA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMO SAPIENS (UDAN),
Udanota, metazoa, chordata, vertebrata; tetrapoda; mammalia;
Utierla; primates.
Score 7; DB 2; Length 109;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8; DB 4; Length 1095;
Pred. No. 1.03e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3DE25EOA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Gaps
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      0
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430 SRSLPLPK 437

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

SEQUENCE 23 AA; 2706 MW;

RESULT

21

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

5 RPSFLLS 11 ||||||| 364 RPSFLLS 370

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Mon Dec 21 09:28:25 1998
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Mon Dec 21 09:28:25 1998

US-08-951-733-14.rept

Page 42

Ouery Match 0.7%; Score 7; DB 2; Length 113; Best Local Similarity 100.0%; Pred. No. 1.01e+01; Matches 7; Conservative 0; Mimatches 0; Indels

0

Caps

0

45 ALRGSGA 51 |||||||| 152 ALRGSGA 158

NON_TER 1 1 NON_TER 113 113 SEQUENCE 113 AA; 11864 MW; 08A79AA1 CRC32;

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63 GASVLGL 69
|||||||
699 GASVLGL 705
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D 004291 PRELMINARY: PRT: 111 AA.
C 004292 PRELMINARY: PRT: 111 AA.
T 01.100Y.1996 (TREMELEEL. 01, CREATED)
T 01.100Y.1996 (TREMELEEL. 02, LAST SEQUENCE UPDATE)
T 01.00Y.1996 (TREMELEEL. 02, LAST ARNOTATION UPDATE)
T 01.00Y.1996 (TREMELEEL. 03, LAST ARNOTATION UPDATE)
T REPORTEDIALA POLITAPPHA (TAST).
T 100ARTOTA, FUNGS: ASCONTROTIAN: HEMIASCONTRETES.
SEQUENCE FROM N.A.
STRAIN-DLI
STR
```

Query Match 0.7%; Score 7; DB 3; Length 111; Best Local Similarity 100.0%; Pred. No. 1.01e+0]; Matches 7; Conservative 0; Hismatches 0; Indels

0 Gaps

6

RESULT: 25

ID GOSSOS. PRELIMINAT: PRT: 117 AA.

AC 035090. PRELIMINAT: PRT: 117 AA.

AC 035090. PRELIMINAT: OL CREATED.

DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMBLEEL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMBLEEL. 01, LAST ANNOTATION UPDATE)

DE U1740A.

PRODUCTION OF TREMBLEEL. 01, LAST ANNOTATION UPDATE)

DE U1740A.

OC PHOGNATORION LEPRAS.

OC PHOGNATORION N.A.

RN SEQUENCE PROM N.A.

RN SEQUENCE PROM N.A.

RN SEQUENCE PROM N.A.

MYCOBACTERIUM LEPRAE.
PROKARTOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.

22 TSRLRFI 28 ||||||| 640 TSRLRFI 646

RESULT: 24

IRESULTATION

PRELIMINAT: PRT: 113 AA.

AD 03.100 PRELIMINAT: PRT: 113 AA.

AD 03.100 PRELIMINAT: PRT: 113 AA.

AD 03.100 PRELIMINAT: PRT: 113 AA.

AD 03.100 PRELIMINATION OF PROME

DT 01.400 1986 (TREMBILEEL. 01, LAST SENGUENCE UPDATE)

DT 01.400 1986 (TREMBILEEL. 01, LAST SENGUENCE UPDATE)

DR 04P217 PRACHEMISTER. 01, LAST SENGUENCE UPDATE)

DR 04P217 PRACHEMISTER. 01, LAST SENGUENCE PRABECIDES;

REPROCHEMISTER, GANCILICUTES; ANOXIPHOTOBACTERIA; PURPLE BACTERIA;

REPROCHEMISTER. 100.1273.

REPROCHEMISTER. 100.107.0622-6431(1995).

PR 250L; US441: 0107109: "THE PRELIMINATION OF PROME AND PROCHEMISTORY OF PROME AND P

Mon

VIRIDAE; SS-RNA ENVELOPED VIRUSES; LENTIVIRINAE. XIANG E., ARIYOSHI K., WILKINS A., DIAS F., WHITTLE H., BREUER J.; ALDS RES. HUM. RETROVIRUSES 13:501-505(1997). EQUENCE FROM N.A. TRAIN-A;

7 PSTSRPP 13 ||||||| | 330 PSTSRPP 336

SEMINERCESO, N.A.
SEMANNECESO, S., KOTANI H., SALUKA T., MITAJIKA I
KAMERO T., TANAKA A., SATO S., KOTANI H., SALUKA T., MITAJIKA I
SEGURAK H., TANAKA A.
SEGURAK S., SATO S., KOTANI H., SALUKA T., MITAJIKA I
BERL, 151-1517A S., SATO S., KOTANI H., SALUKA T., MITAJIKA I
SEGURACE T., SALUKA A., SATO S., KOTANI H., SALUKA T., MITAJIKA I
SEGURACE T., SALUKA A., SATO S., KOTANI H., SALUKA T., MITAJIKA I
SEGURACE T., SALUKA T., SALUKA T., SALUKA T., MITAJIKA I
SEGURACE T., SALUKA T. LLOGGI. WECHCCTSTIS SP. ROKARTOTA; BACTERIA; GRACILICUTES; OXYPHOTOBACTERIA; CYANOBACTERIA; RROCCOCCALES.

Ouery Match 0,7%; Score 7; DB 14; Length 125; Best Local Similarity 100 0%; Pred No. 1 Ole+01; Matches 7; Conservative 0; Mismatches 0; Indels 0;

ö

Caps

Query Match 0.7%; Score 7; DB 2; Length 128; Best Local Similarity 100.0%; Pred. No. 1.01e+01;

US-08-951-733-14.rspt

POSITIVE-STRAND; RETROVIRIDAE;

STRAIF-A:
STRAIF-A:
STRAIF-A:
GRASSIY N. XIANG E., ARIYOSHI K., AABY P., JENSEN B., DIAS P.,
WHITTLE R., BREUER J:
SURNITTED (NAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AJ008512: E129784;
NOR_TER 125 125
NOR_TER 125 A): 1355 NH; PC04002C CRC32:
SEQUENCE 125 AA: 13505 NH; PC04002C CRC32:

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US-08-951-733-14.zspt

D 073111 PRELIMINARY; PRT; 125 AA.

C 073111 PRESIDENT. 07, CREATED;
T 01-NG-1980 (TREMSLEEL. 07, CAST SECURING UPDA)
T 01-NG-1980 (TREMSLEEL. 07, LAST AUROTATION UP
C 0AG PROTEIN (TRAGERY).

H 0AG.

CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)

Query Match 0.7%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 2; Length 117; Pred. No. 1.01e+01; 0; Mismatches 0; Indels

..

Caps 0 SEQUENCE FROM N.A.
ROBISON K.;

MITH D.R.; DEMITTED (APR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS

65 ARRRGGS 71 ||||||| 243 ARRRGGS 249

9

7; Conservative 0 Mismatches 0; Indels 0; Caps

46 AVVIEQS 52 |||||||| 811 AVVIEQS 817

RESCUTA 18

TO 080929 PRELIMINARY, PRT: 135 AA.

AC 080929 PRELIMINARY, PRT: 135 AA.

AC 080929 PRELIMINARY, PRT: 135 AA.

TO 101807-1996 (FRESDLEEL 01. LAST SECRETE UPDATE)

DT 01.807-1996 (FRESDLEEL 01. LAST SECRETE UPDATE)

TO 1807-1996 (FRESDLEEL 01. LAST SECRETE UPDATE)

DE 7-CELL LEVENDATA-INFERONA VIRUS TYPE II (CLONE NO-6) 7AX-2 (FRACKENT).

ON TAX-2.

ON TRANSLES SERVA NONEXPELDEDE DIRECTES, POSITIVE STRAND RNA VIRUSES;

ON CHINARY, SERVA NONEXPELDEDE DIRECTES, POSITIVE STRAND RNA VIRUSES;

ON CHINARY, SERVA NONEXPELDEDE DIRECTES, POSITIVE STRAND RNA VIRUSES;

ON CHINARY, SERVA NONEXPELDEDE ORGOVIRUS GROUP;

ON MANGALLAN TIPE CONCOVIRUSES.

RN 11)

RN 12122 B. CCAMET R.;

FR MEDIATE 3236016:

RN 12122 B. CCAMET R.;

FR MEDIATE 135 AA; 14124 MN; 1885401E CRC32; SECURNCE FROM N.A.
MEDILIES, 223616.
MINILIES, CHANET R.,
J. MED. VIROL, 36:135-141(1992).
DEBL: #8388; G129556; -.
NOM_TER 5186; G129556; -.
SECURNCE 135 AA; 14124 MM; 1885402E CRC32;

O-7s; Score 7; DB 14; Length 135; Best Local Similarity 100 0%; Prof. No. 1 De+01; De-02; Conservative 0; Hismatches 0; Indels 0; Caps

72 SRSLPLP 78 ||||||| 251 SRSLPLP 257

108023 PRELIMINARY PRT. 138 AA.
080823 PRELIMINARY PRT. 138 AA.
080823 PREMIMER. 01, CREATED)
01-NOV-1996 (TREMGLERI. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMGLERI. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMGLERI. 01, LAST SHOOTATION UPDATE)
01-NOV-1996 (TREMGLERI. 01, LAST SHOOTATION UPDATE)
101-NOV-1996 (TREMGLERI. 01, LAST SHOOTATION UPDATE)
111-NOV-1996 (TREMGLERI. UPD

SEQUENCE PROM N.A.

Paga 44

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RESULT 33

ID 09335;

OR 09335;

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RESULT
ID Q8
AC Q8
DT 01
DT 51
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          Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0,7%; Score 7; DB 2; Length 146; Best Local Similarity 100.0%; Pred. Mo. 1.01e+01; Indels Matches 7; Conservative 0; Mismatches 0; Indels
117 14 A.
082391 PRELIMINARY, PRT: 149 AA.
082392 PREMIMENT, O1, CREATED)
01.WOV-1996 (TREMBLEEL, O1, LAST SEQUENCE UPDATE)
01.WOV-1996 (TREMBLEEL, O1, LAST SEQUENCE UPDATE)
01.UTW-1996 (TREMBLEEL, O5, LAST MANOTATION UPDATE)
17-CELL IMPROTROPIC VIRUS TIPE 2 REX AND TAX GENES,
572 (TRANSMERT)
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082405, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 082406, 0824
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CIMINALE V. D'AGSTINO D.M., ZOTTI L., FRANCHI CHIEDO-BLANCHI L.;
CHIEDO-BLANCHI L.;
VIROLOGY 209:445-456(1995),
EMBL. L14156; G780299; .
SEBUL L14156; G780299; .
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372 LRPSLTG 378
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EMBL; D63524; 6340401; -
EMBL; D63524; 6340401; -
EMBLYTER 146 146
EMBLYTER 146 146
EMBLYTER 146 AA; 16712 NH; 53345260 CRC32;
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048981 PRELIMINARY; PRT: 146 AA.
048981, 1996 (TREMELREL. 01, CREATED)
01:WOY-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
01:WOY-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
01:WOY-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
10:WOTO-1996 (TREMELREL. 07, LAST ANOTATION UPDATE)
10:ATROPELM (FRACEMES:
10:ATROPELM (FRACEMES)
10:ATROPELM (FRACE
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251 SRSLPLP 257
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251 SRSLPLP 257
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KEDLINE; 9619054.

KEDLINE; 9619054.

LOUVIERA M.D., OLIVIERA O.D., ISHAK R.,

CLIVIERA M.P., LADREIRO P., ISHAK M., ACEVEDO V., BANDERSHAK R.,

TURO T., PALL M.M.;

J. VEROL. 70:14811192(1996).

ENGL. 70:14811192(1996).

KENT. 70:2873; G146304; ...
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VIRIDAE; SS-RAK NONEWYELOPED VIRUSES; POSITIVE STRAKD RHA VIRUSES;
RETROVIRIDAE; DECOVIETINE, TYPE C ONCOVIRUS GROUP;
MANMALIAN TYPE C ONCOVIRUSES.
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TRAIN=W70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7: DB 14: Length 138;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANCHINI G., PELBER B.K.,
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                                                                                                  PARTIAL CDS,
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Query Match

0.7%; Score 7; DB 14; Length 149;

SECURME PROM N.A.
MEDLINE: 9619054.
MEDLINE: 9619054.
METAGU N. NOVOA D., NONKEN C., OLIVIERA M.D., OLIVIERA O.D., ISHAK
COLIVIERA M.P. LAURETRO D., ISHAK M., ACPYEDO V., HAMMERSHLAK N.,
EUU R.M., NEDO 1.14914.1991.
EMBL. 013887; 1465063; "."
EMBL. 013887; 1465063; "."

CDS,

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RESURGATION

RESURGATION

RESURGATION

AC 083408

DT 01-NOV-1996 (TREMELEEL, 01, CREATED)

DT 01-NOV-1996 (TREMELEEL, 02, LAST ANDURICE OPDATE)

DT 01-NOV-1996 (TREMELEEL, 03, LAST ANDURICE OPDATE)

DT 7-CELL LYMPHOYROPIC VIRUS TYPE 2 REX AND TAX GENES, PARTIAL CDS

DE TUC BY (FRANCEIST)

OF RESULTANCE PROPERTY OF THE TYPE 1 REX AND TAX GENES, PARTIAL CDS

OF RESULTANCE SEARCH NORWENGLED BY LEGISLES OF THE STAND RAN VERGIS

OC REPROVIENDAE, ONCOVIRINAE; TYPE C ONCOVIRUS GROUP;

OF MANDALIAN TYPE C ONCOVIRUSES.

RY ELINE, 96190544.

RA ELIALU N. NOVAD P. HONKEN C., OLIVIERA H.D., OLIVIERA N.D., 11

RA CHUTERA M.P., LAWREITO P., ISHAK M., ACEVEDO V., HAMMERISHIAN R. LAWREITO P., 15HAK M. P.

RA LEIGHD 1368; 01461-0431.

RA LEIGHD 1368; 01461-0431.

RA DEBU UN 1361-1461-0431.

END MED 1362 1461-1461-0431.

END MED 1362 1461-1461-0431.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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251 SRSLPLP 257
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NON_TER 1 1
SEQUENCE 149 AA; 15672 MW;
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STRAINESP2 PR.
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SENDIMENEAURAD GIAVA) PX:

SENDANG N. BOOKOA P., HONKEN C., OLIVIERA M.D., OLIVIERA O.D., ISHAK R.,

BIRAKU N. BOOKOA P., HONKEN C., OLIVIERA M.D., OLIVIERA O.D., ISHAK R.,

BIRAK M.P., LAUDEERO P., ISHAK M., ACEVEDO V., HAMMERSHLAK N.,

ENG S.N., KIED I., SHLL N.W.,

J. VIROL. 70:1481-14921(1995).

EMBL. UJ2074; G145004; -.
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251 SRSLPLP 257
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MEDLINE: 9619054.
MEDLINE: 9619054.
OLIVIERA N.B., NOVA, P., NONERS C., OLIVIERA N.D., OLIVIERA O.D.,
CHIVIERA N.P., LADREITEO P., ISHAK M., ACEYEDO V., HAMCERSHLAK
TURS N., KURO T., NALL M.W.;
TURS N., TURS N., NALL M.W.;
TURS N., TURS N., NALL M., NALL M.W.;
TURS N., TURS N., NALL M., NALL M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.
VIRIDAE: SS-RNA NOMENVELOPED VIRUSES: POSITIVE STRAND
RETROVIRIDAE: ONCOVIRUNE: TYPE C ONCOVIRUS GROUP;
MANDALIAN TYPE C ONCOVIRUSES.
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VIRIDAE, SS-RMA NOMENVELOPED VIRUSES, POSITIVE STRAND RNA
RETROVIRIDAE, ONCOVIRINAE, TYPE C ONCOVIRUS GROUP;
MAMMALIAN TYPE C ONCOVIRUSES.
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REX.
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 14; Length 149;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5E356C3B CRC32;
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Page 48

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86 SRSLPLP 92 ||||||| 251 SRSLPLP 257

Best Local Similarity 100.0%; Pred. No. 1.01e+01; Matches 7; Conservative 0; Hismatches 0;

US-08-951-733-14.rapt

Caps

Page 49

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OMBELLIFERAE.

US-08-951-733-14.rspt

AT THE GLOBULAR STAGE;

Page 50

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RESULT 18

                                                                                                                                          RESULT 40

ID 073454

AC 073454

DT 01-MG-1998 (TREDBLEEL, 07, CREATED)

DT 01-MG-1998 (TREDBLEEL, 07, LAST SEGUENCE UPDATE)

DT 01-MG-1998 (TREDBLEEL, 07, LAST SEGUENCE UPDATE)

DT 01-MG-1998 (TREDBLEEL, 07, LAST ANNOTATION UPDATE)

DE REX PROTEEL.

GN REX.

OS HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2BIV-HTLV RETROV

CC WINDESS; RETROID VIRUSES; RETROVIBLIAE, BLV-HTLV RETROV

CC EUMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2.

RH (11)

RH SEQUENCE FROM N.A.

RD LETTOMBEUR F., D'ADRIOL L., DAZEA M.C., PETEZRS M., BED

RA LETOMBEUR F., D'ADRIOL L., DAZEA M.C., ANNELAISIR N.;

RH SEQUENCE FROM N.A.

RH SEQUENCE FROM N.A.

RH SEQUENCE FROM N.A.

RH SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

11051; ELSG5011.
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11 039680
AC 039680; PRELHHARY: PRT; 153 AA.
AC 039680; PRESIDENCE. 01, CREATED;
DT 01-NOT-1996 (TREMELEEL. 01, LAST SEQUENCE UPDATE)
DT 01-NOT-1996 (TREMELEEL. 07, LAST SEQUENCE UPDATE)
DT 01-NOT-1996 (TREMELEEL. 07, LAST ANNOTATION UPDATE)
DE REAT-SECUE COGNATE (TRAGEET)
OS DAUCUS CAROTA (CARROT).
OS DAUCUS CAROTA (CARROT).
OC EURARYOTA: PLANTA: EMERYOPHYTA; ANGIOSPENAE; DICOTTLEDONEAE; AFIALES;
OC EURARYOTA: PLANTA: EMERYOPHYTA; ANGIOSPENAE; DICOTTLEDONEAE; AFIALES;
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Best Local Similarity 100.0%;
Matches 7; Conservative
     Query Match 0.7%; Score 7; DB 14; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.01e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 7; Conservative
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01.-TUL-1997 (TREMSLERL, 04, CREATED)
01.-TUL-1997 (TREMSLERL, 04, LAST SEQUENCE OPDATE)
01.-TUL-1997 (TREMSLERL, 05, LAST ANNOTATION OPDATE)
SINAPORETRI HOMOLOG.
BIRHOD MEDICANALIS (MEDICINAL LEECH)
UDGARTOTA: METALOA; ANNELIDA; HIRUDINEA.
(1)
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TISSITEMENTS CORD:
TUSSITEMENTS CORD:
BRUNS D. ENERGY S. YANG C., OSSIG R., JEROMIN A.,
J. MEJEROSCI, 17:1899-1910.1997).
EMBL, 05505; 01202350; ...
EMBL, 05505; 01202350; ...
SEQUENCE 169 AA: 17817 MM; P4C05E4B CRC32;
                                                                                                                                     SEQUENCE PROM N.A.
LETOTRIBETH F.
LETOTRIBETH F.
SUBMITTED (NAY.1997) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL. Y11051; E.
EMBL. 
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[[|||||
237 GLPAPGA 243
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151 SRSLPLP 257
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STRAIN-EMAND (16A1) PX:
REDLINE: 96190544.
EIRAKU N. NOVAD P., HONKEN C., OLIVIERA H.D., OLIVIERA O.D., ISHAK R.,
EIRAKU N. NOVAD P., HONKEN C., OLIVIERA H.D., OLIVIERA K.P., LAURENG P., ISHAK K., ACEVEDO V., HAMERSHIAK N.,
EHU S.W., KURD C., 19614 M.F.;
EMBL., 2017-1481-1482(1986).
MEML., 2017-1481-1482(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 1 .
SEQUENCE 149 AA; 15779 MW; 5E356C3B CRC32;
                                                                                                                                                                                                                                                                                                                                                                            DÉDURCE FROM N.A.
METODURUET E. D'AURIOL L., DAZZA M.C., PETERS M., BEDJABAGA
'YOT P., DELAPORTE E., GESSAIN A., MONPLAISIR N.;
GEN. VIROL. 79:269-277(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAN T-CELL LYMPROTROPIC VIRUS TYPE 2B.
RUGES, RETROUD VIRUGES; RETROVIRIDAE; BLV-HTLV RETROVIRUSES;
MAN T-CELL LYMPHOTROPIC VIRUS TIPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 14; Length 149;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 5; Length 169;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-951-733-14.xept
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TO 405501: PRELIMINARY; PRT: 170 AA.

TO 01-NOV-1996 (TREMBLREL 01, CREATED)

TO 11-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)

TO 11-NOV-1996 (TREMBLREL 01, LAST ANOTATION UPDATE)

TO 11-NOV-1996 (TREMBLREL 01, LAST ANOTATION UPDATE)

BENTAN TO-CLIL LIMINATOROPIC VIRUS TIPE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ş
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ID 001388
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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|||||||
|892 DGLLLRL 888
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STRAND-DAVER HALF-LONG, TISSUE-SOMATIC EMBRYOS AT TH
LIN X., HAANG G.J., ZIMMERWAN J.L.,
SUBMITTED (JAN-1996) TO EMBL/CENBANK/DDBJ DATA BANKS.
FABL: G47094 G.175945].
FPAM: PPOODIJ: HEPPO.
NON_TER
15 103 AA; 18394 MN; A7D65CA5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                        107 SRSLPLP 113
|||||||
251 SRSLPLP 257
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QUORDS

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251 SRSLPLP 257
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|||||||
401 LPRLPQR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDILER: 9316343.
MEDILER: 9316343.
MEDILER: DIDLER N.B. SEANSON P., ADARTICIO J.J., CHIN N.N., LAX J.P.,
MEDILER: DIDLER N.B. SEANSON P., ADARTITI A., MARINUCCI G., CHEN I.S.Y.,
MEDILER: DIDLER: D. SEANSON P., ADARTITI A., MARINUCCI G., CHEN I.S.Y.,
MEDILE: LILI145; G34840; ...
EMBL: LIJ145; G34840; ...
EMBL: LIJ153; G3464041.
EMBL: LIJ073; G464041.
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EMBL; 273147; E245470; -
SEQUENCE 167 AA; 19759 MW; SABBF574 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEPORESE PROM N.A.
MEDLIER, 9933307
NARDI D., SMITZER H.M., HADLOCK K.G., KAPLAN J.E., LAL R.B.,
VARDI D., 67:4659-4664(1993).
J., VIROL. 67:4659-4664(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN T-CELL LEUKEMIA VIRUS TYPE II (ISOLATES G12 AND NRA) (HTLV-II).
VIRIDAE; SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESOURNES FROM N.A.
HEDLER H., WEDLER E., SCHARPE M., WAMBUTT R.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 14; Length 170;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 3; Length 167;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7: DB 10: Length 153;
Pred. No. 1.01e+01:
0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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ID 056935 PRELIMINARY;
AC 056935 PRELIMINARY;
AC 056935.
DT 01.90V.1996 (TREMBLREL. 0
DT 01.90V.1996 (TREMBLREL. 0
DT 01.90V.1996 (TREMBLREL. 0
DE VOPK. 1996 (TREMBLREL. 0
DE VERT. 05 VERT. 05 VERT. 05 VERT. 05 VERT. 05 VERT. 05 VERT. 06 VERT. 06 VERT. 06 VERT. 06 VERT. 06 VERT. 07                                             Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                   SECUENCE FROM N.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
WHITE D., CLATYON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
SUBHLITZED (SEP-1995) TO DOBL/GENBANK/DDBJ DATA BANKS.
ENDL. U32841: G1544515; TO DOBL/GENBANK/DDBJ DATA BANKS.
SECUENCE 193 AA: 20590 NM; 43A5EB6A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 09:28:25 1998
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| | | | | | | |
251 SRSLPLP 257
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ROSENBLATT:
ROSENBLATT:
ROSENBLATT:
ROSENBLATTED (NOV-1986) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: ALONGO:
SEQUENCE 170 AA: 18463 MF; 00011EBJ CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECURNCE FROM N.A.

MEDLINE: 82134-49.

SHIMOTONIO I. TAKANSHI Y. SHIMIZU N., GOJOBORI T.,

CHEN I.S. HIMA M. SUGLMUBA T.,

PROC. NATL. ACAD. SCI. U.S.A. 82:3101-3105(1985).
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MEDILINE: 8425019
SCHEMENT D., BRIGGS D., LEZ T.H.,
COLIGAN U., PONG-STAML F., GALLD R.C., BASELTINE W.A.;
SCHEMEZ 225-41-424(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TERSINIA PERDOPUBERCULOSIS.
PLASHID PIB.
PROKARYOTA; GEACILICUTES; SCOTOBACTERIA; PACULTATIVELY ARAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRIDAE: SS-RA, NORENYELOPED VIRUSES; POSITIVE STAND RM. VIRUSES;
RETROVIRIDAE: ONCOVIENUAE: TYPE C ONCOVIRUS GROUP;
NAMPALIAN TYPE C ONCOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESPODENCE PROM H.A.

WEISS R.L., TEICH H., VARHUS H., COPPIN J.J. (EDS.);

(IN) WEISS R.L., TEICH H. VARHUS H., COPPIN J. (EDS.);

RAM, TUMON VIEWESS, SECOND EDITION, J. VOL. 2.1070-1085;

COLD SPRING HARBON LADORATORY, COLD SPRING HARBON (1985);
                                                                                                                                                                                                                                                                                                                                  EXECUENTA R. D., ADMAS M. D., HEITE O., CLAYTON R.A., KIRKHESS R.P., EXEMBER, R. BULT C.J., TOWN J.F., DOGGERETI R.A., MERIKICI J.M., PRELIX G.A., CANTER J.D. M. PERIKICI J.M., PRELIX G.A., CANTER J.D. M. HEIDMAN J.F., DOTT. J.D., SHIRLER R., LULLI, GLODEK A., EXILEY J.M., HEIDMAN J.F., MILLEY G.M., PREIDMAN J.F., MAN, M.C., PROPER J.C., PRESENCE, R. BRANCON R.C., PERE L.D., ROYALD J.T., FURRMANN J.M., SECONIAGEM M.G.M., GNEIM E.L., DANASCE, CH., SHITH R.C., VENTER J.C., EMPACE J.C., PRESENCE J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PÓURICE PROM N.A.

TATUSOV R., MUSHECIAN A.R., BORK P., BROWN N.P.,

PRODOVSKY M., RUDD K.E., KOONIN E.V.;

PR. BIOL. 6:279-291(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOLINCE FROM N.

DILINE; 935061.

ELSCEMANUR D. D. ADASS H. D., WHITTE O., CLAYTON R.A., KIRKNESS E.F.,

ELSCEMANUR D. D. ADASS H. D., WHITTE O., CLAYTON R.A., KIRKNESS E.F.,

ELAVAGE A. R., BUTC C.J., TOMB J.F., DOUGHERT B.A., MERRICK J.H.,

KERNEY K. SCOTTON C. TITHERIGH W., PIELS C.A., CAVIET J.D.,

DOTT J.D., SHIKLEY R., LIU L.I., GLODER A., KILLEY J.M., WEIDMAN J.F.,

TILLIPS C.M., SPRIGES T., HENDEAM R., CHALLEY J.M., MEIDMAN J.F.,

NURA M.C., MOTEN D.T., SAUDEK D.M., BRANGON R.C., FIRE L.D.,

TOMBALD L.A., SENALLE K.V., GROCHGEM N.S.M., GRENS C.L.,

DONALD L.A., SHALLE K.V., GROCHGEM N.S.M., GRENS C.L.,

JIENCE 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTHEPICAL.
1683.
BARDHILIS INFLUENSAE.
BANDHICAS GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
STONELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FEB-1997 (TREMBLREL
-FEB-1997 (TREMBLREL
-AUG-1998 (TREMBLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUENCE FROM N.A.
EISCHMANN R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555
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Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                 Score 7; DB 2; Leng
Pred. No. 1.01e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
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                                                                                                      Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAYES W.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOLDE D.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESSEX
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5 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEDLINE; 9526274.
HOLMSTROM A., ROGUVIST R., WOLF-WATE H., PORSBERG A.;
INFECT. IMMUN. 63:2269-2276(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SĒQUENCE FROM N.A.
ROLMSTRYM A.H.;
SUBMITTED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA
EMBL, D18804; G619941; -.
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Dec

70 TPLRTLV 76

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RESULT 44

D 668704 PRELIMINAT: PRT: 182 AA.

D 668704 PRELIMINAT: PRT: 182 AA.

D 668704 PRELIMINAT: PRT: 182 AA.

D 668704 PRELIMINAT: O, CSEAIED)

D 10.AGC-1998 (TREMBLEEL O, LAST SECUENCE UPDATE)

D 10.AGC-1998 (TREMBLEEL O), LAST SECUENCE UPDATE)

D 10.AGC-1998 (TREMBLEEL O), LAST ANNOTATION UPDATE)

D 10.AGC-1998 (TREMBLEEL O), LAST AGC-1998 (TREMBLEEL O), LAST AGC-1998 (TREMBLEEL O), CARNES D, SECUENCE (TREMBLEEL O), ANNOTATION UPDATED (TREMBLEEL O), AND CREADY P., SECONDONSKI E.; CANNES D, RESULT AF CARNES D, SECONDON UPDATED (TREMBLEEL O), AND CREADY P., SECONDON UPDATED (TREMBLEEL O), AND CREADY P.
Dec 21 09:28:25 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 0.1%; Score 7; DB 2; Length 182; Best Local Similarity 100.0%; Pred. No. 1.01e-01; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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005503

PRELIMINARY;

005503;

01-JUL-1997 (TREMBLREL.)

01-JUL-1997 (TREMBLREL.)

01-JUN-1998 (TREMBLREL.)

01-JUN-1998 (TREMBLREL.)
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|||||||
856 GSILSTL 862
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SEQUENCE 182 AA; 21000 MW; ADB431D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 GSILSTL 68
|||||||
856 GSILSTL 862
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STRAIM-RIM:
HU P., ELLIOTT J., MCCREADY P., SKOWRONSKI E.; GARNES J.,
HU P., ELLIOTT J., MCCREADY A.V., BRUBAKER R., CARCIA E.;
KORANSHI A., CARCANO A.V., BRUBAKER R., CARCIA E.;
SUBMITTED (MATTED) (M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGASAWARA N.;
SUBMITTED (APR-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=168;
SADAIE Y., YATA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEONEMER FROM N.A.
SEONEMER FROM N.A., SOUTTA M., SAGAI H., ITAYA M., KASAHARA
SAGARARAN M., PUTTA K., PUTTA M., SAGAI H., ITAYA M., KASAHARA
GURNITITED (APR-1997) TO EMEL/GENBANK/DDBJ DATA BARKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904 TELETLY 910
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PAGMID PODI.
PROMINOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CILLUS SUBTILIS.
OKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., YATA K., PUJITA M., SAGAI H., ITAYA M., KASAHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    김
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 2; Length 182;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 AA.
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848888 848888

WILKINSON-SPROAT J., WOHLDM MATURE 368:33-38(1994). EMEL: E48045: E348246: -HYPOTHETICAL PROTEIN. NON_TER 206 206

WOHLDMAN P ..

SEQUENCE 206 AA;

206 23256 MW; ODF4ED1E CRC32;

8

Query Match 0.7%; Score 7; DB 5; Length 206; Best Local Similarity 100.0%; Pred. No. 1.01e+0; Matches 7; Conservative 0; Mismatches 0; Indels

9

Caps

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Mon
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                                                                          Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Overy Match 0.7%; Score 7; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. Mo. 1.01e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ULT 49

950447 PRELIMINARY;

050447;

01-NOV-1996 (TREMBLREL 01, C

01-JAN-1998 (TREMBLREL 05, I

01-UN-1998 (TREMBLREL 06, I
110 KELVARV 116
|||||||
100 KELVARV 106
                                                                                                                    ILT 47

1018560 PRELIMINARY: PRT; 206 AA.

101850: CREATED;
101-NOV-1998 (TREMBLEEL. 01. CREATED)
101-NOV-1998 (TREMBLEEL. 07. LAST AUMOTATION UPDATE)
101-NOV-1998 (TREMBLEEL. 08. LAST AUMOTATION UPDATE)
101-NOV-1998 (TREMBLEEL. 09. LAST AUMOTATION UPDATE)
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735 VIGAYDT 741
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STRAIN-169
STRAIN-169
STRAIN-169
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STRAIN-169
TO EMBL/GENBANK/DEBU DATA BANKS.
EMBL. 189100; 18100549
SEQUENCE 205 AA; 22536 MY; 61C12275 CRC32;
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TANANASHI H., TAKENANI K., TAKENGIK H., TAMANGII A., TANAKA T.,
TERBYTRA P., TOCARONI A., TOSATO V., UCHITANA S., VANDEZEBOL H.,
VANNIZE P., VASAROTI A., VIARI A., VANDUTE R., VEDLER E., WEDLER E.,
TASTROSGER T., NIFFESS P., WIPAT A., YAMANOTO H., TANAE K.,
TASHROTO K., TANA K., YOSHIJA K., YOSHIJANA H.P., ZUMSTEIN E.,
TOSHIJANA H., DARCHIM A.,
MATURE 190:143-236(1997).
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ILLEON R., AINSCOUGH R., ANDERSON K., BANNES C., BERKS M., BONFIELD J.,

ULTON R., AINSCOUGH R., ANDERSON K., CONDEN J., COLLON R., CRATON M.,

URTON J., CONNELL M., COPERT T., COOPER J., COLLON R., CRATOR M.,

URACA S., DO E., DORBIN R., FAVELLO A., FULTON L., CARDNER A., GERS P.,

LARRIES T., HILLER L., JIER M., JOHNSON M., LIOTD C.,

URSTEN J., LATSTER N., LATRELLLE P., LICHTNING J., LLOTD C.,

CHORRAN A., MORTHANCE D., COLLLAGAM N., PARSON J., PERT C.,

CHORRAN A., MORTHAN R., SAUNDESS D., SHONKESM R., SMALDON N., SMITH A.,

VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,

VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
TRAIN-H37RV;
EDLINE; 96181548.
                                                                                                                                                                                                                                                                                   IDLINE; 96236050.
                                                                                                                                                                                                                                                                                                                                                                                                                 EDLINE: 96181548.
EDLINE: 96181548.
HILIPP W.J., POULET S., EIGLMETER K., PASCOPELLA L.,
ALASUBRANANIAN V., HETM B., BERGH S., BLOOM B.R., JACOBS W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE PROM N.A.
TRAIN=H37RV;
DCOCK K., CHURCHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eddence from N.A.
URTON J.;
DISMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCOCK K., CHURCHER C.M.;
PARITIED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NENORHABDITIS ELEGANS.
NARYOTA: METAZOA; ACOELOMATES; NENATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                      QUENCE OF 4-228 FROM N.A. RAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COBACTERIUM TUBERCULOSIS:
OKARYOTA: FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE S.T., BARRELL B.G., RAJANDREAM M.A.;
BMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09:28:25 1998
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                                                                          Score 7; DB 2; Length 228;
Pred. No. 1.01e+01;
0; Mismatches 0; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 AA.
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                                                                             0; Indels
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RESULT

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Search completed: Fri Dec 18 18:47:31 1998 Job time: 205 secs.

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RESULT. 48

DESCRIPT. 48

DESCRIPT. 48

DESCRIPT. 49

DESCRIPT. 40

DESC
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                                                                                                                                                                                                                Query Match 0.7%; Score 7; DB 2; L
Best Local Similarity 100.0%; Pred. No. 1.01e+01
Matches 7; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 1.01e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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147 REAGVPL 153
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230 REAGVPL 236
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69 FRALVAQ 75
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827 LPDVPLR 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 231 AA; 24338 MW; 0529956C CRC32;
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069113 (TREMBLEEL O, CRANTS)
01.AUG-1998 (TREMBLEEL O, LAST SEQUENCE UPDATE)
01.AUG-1998 (TREMBLEEL O, LAST SAUDENCE UPDATE)
01.AUG-1998 (TREMBLEEL O, LAST SAUDTNION UPDATE)
01.AUG-1998 (TREMBLEEL O, LAST SAUDTNION UPDATE)
020ATVE DIFFLORONCYASE (FRANCET)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOURNCE FROM N.A.
STRAIN-10265.
STRAIN-10265.
DESHAER D.M. T-1958) TO EMBL/GENBANK/DDBJ DATA BANKS
SUBMITTED (MY 1-1958) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBLY_RF064070; G3135671; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BURKHOLDERIA PSEUDOMALLEI.
EUBACTERIA: PROTEOBACTERIA: BETA SUBDIVISION; BURKHOLDERIA.
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                                                                                                                                                                                                                                                                                                                                         Length 231;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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### Additional Control Real Type I indoctive	Mon Dec 21 09:28:26 1998 US-08-951-733-20.xag	150 6	Mon Dec 21 09:28:26 1998 US-08-951-733-20.xag
	Page 7		Page 5
302 6 0.5 334 23 W22177 S.thermophilus exampol 5.54e-02 372 6 W20431 Sequence of orbits II. 5.54e-02 372 8 W20431 Sequence encoded by s. 5.54e-02 372 8 W20431 Sequence encoded by s. 5.54e-02 372 8 W20431 Sequence encoded by s. 5.54e-02 372 8 W20431 Canibs II.12 P40 subb 5.54e-02 372 8 W20431 Canibs III.12 P40 s	Non Dec 21 09:28:26 1998 US-08-951-733-20.rag	201 6 0.5 207 2 Mil288 Mouse oligodendrocyte 5.54e-02 202 6 0.5 211 9 Mil200 Christophendrocyte 5.54e-02 203 6 0.5 211 9 Mil200 Christophendrocyte 5.54e-02 204 6 0.5 211 9 Mil200 Christophendrocyte 5.54e-02 205 6 0.5 214 4 P99468 Sequence moded by 5.54e-02 206 6 0.5 214 2 P99468 Sequence moded by 6.54e-02 207 6 0.5 214 2 P99469 Sequence moded by 6.54e-02 208 6 0.5 214 2 P99469 Sequence moded by 6.54e-02 209 6 0.5 214 2 P99469 Sequence moded by 6.54e-02 214 6 0.5 215 1 Mil200 Animophil derived bat 6.54e-02 215 6 0.5 222 P99469 Sequence moded by 6.54e-02 216 6 0.5 222 P99469 Sequence moded by 6.54e-02 217 6 0.5 222 P99469 Sequence moded by 6.54e-02 218 6 0.5 222 P99469 Sequence moded by 6.54e-02 219 8 180110 Animophil derived bat 6.54e-02 219 8 180110 Animo acid sequence 6.55e-02 220 8 1 Mil200 Animophil derived bat 6.54e-02 221 8 180471 Animo acid sequence 6.55e-02 222 8 180471 Animo acid sequence 6.55e-02 223 1 Mil200 Animophil derived bat 6.55e-02 224 1 Mil200 Animophil derived bat 6.55e-02 225 1 Mil200 Animophil derived bat 6.55e-02 226 6 0.5 213 1 Mil200 Animo acid sequence 6.55e-02 227 8 1 Mil200 Animo acid sequence 6.55e-02 228 1 Mil200 Animo acid sequence 6.55e-02 229 8 1 Mil200 Animo acid sequence 6.55e-02 220 8 1 Mil200 Animo acid sequence 6.55e-02 221 8 Mil200 Animo acid sequence 6.55e-02 222 8 Mil200 Animo acid sequence 6.55e-02 223 1 Mil200 Animo acid sequence 6.55e-02 224 1 Mil200 Animo acid sequence 6.55e-02 225 1 Mil200 Animo acid sequence 6.55e-02 226 1 Mil200 Animo acid sequence 6.55e-02 227 1 Mil200 Animo acid sequence 6.55e-02 228 1 Mil200 Animo acid sequence 6.55e-02 229 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 220 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 221 Mil200 Animo acid sequence 6.55e-02 222 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 223 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 224 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 225 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 226 6 0.5 221 Mil200 Animo acid sequence 6.55e-02 227 6 0.5 221 Mil200 Animo acid sequence 6.	Non Dec 21 09:28:26 1998 US-08-951-733-20.zag

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	Page 11		Page 9
SOT CONTINUENTS CONTINUENTS SECRETARY SECRETAR	Mon Dec 21 09:28:26 1998 U9-08-951-733-20.rag	### Ruman plasma carboxyp 5.54e-02 ### Ruman interstantin-13 ### Ruman interstantin-13 ### Ruman interstantin-13 ### Ruman interstantin-15	Man Dec 21 09:28:26 1998 US-08-951-733-20.reg

500 6 0.5 822 5 R25337 F.g. and S. Selevico S. Selevic	Man Dec 21 09:28:26 1998 US-08-951-733-20.xeg	\$550 6 0.5 5521 PR2576 National Requestor from 5.54e02 \$560 6 0.5 552 A WARDEN Steen From 5.54e02 \$561 6 0.5 552 A WARDEN Steen From 5.54e02 \$562 6 0.5 552 A WARDEN Steen From 5.54e02 \$563 6 0.5 552 A WARDEN Steen From 5.54e02 \$564 6 0.5 552 A WARDEN Steen From 5.54e02 \$565 6 0.5 552 A WARDEN Steen From 5.54e02 \$567 6 0.5 552 A WARDEN Steen From 5.54e02 \$568 6 0.5 552 A WARDEN Steen From 5.54e02 \$569 6 0.5 552 A WARDEN Steen From 5.54e02 \$560 6 0.5 55	Man Dec 21 09:78:26 1998 US-08-951-733-20.zag
	Page 15		Page 13
711 6 0.5 1146 3 R15156 Abelson Related Gene. 5.54e+02 712 6 0.5 1185 2 R35209 Archica dempty 24 cycl. 5.54e+02 713 6 0.5 1186 28 R42591 Anisoa Call acquinose 5.54e+02 714 6 0.5 1126 2 R42591 Anisoa Call acquinose 5.54e+02 715 6 0.5 1215 2 R42591 T19120 5.54e+02 716 6 0.5 1215 2 R42591 T19120 5.54e+02 717 6 0.5 1245 2 R43592 Bacillus thuringiensi 5.54e+02 718 6 0.5 1245 2 R43592 Bacillus thuringiensi 5.54e+02 719 6 0.5 1245 2 R43592 Bacillus thuringiensi 5.54e+02 719 6 0.5 1245 2 R43592 Bacillus thuringiensi 5.54e+02 710 6 0.5 1245 2 R43592 Bacillus thuringiensi 5.54e+02 711 71	Man Dec 21 09:28:26 1998 Us-08-951-733-20.zeg	800 6 0.5 883 6 RAISSI 801 802 803 6 RAISSI 802 803 607 18 RESERVING CHARACTER CONTROL	Mon Dec 21 09:28:26 1998 U8-08-951-733-20.rag
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0.4 464 8 R43905 Ruman antithrombin II 4 0.4 465 13 R66738 Anti-tobacco mosaic v	### 5 0.4 331 16 R90771 Bacillus stearctherm 0.83e+03 ### 65 5 0.4 331 2 R32315 Recombinant hematopoid 4.83e+03 ### 66 5 0.4 332 4 R32359 Recombinant coupled hum 4.83e+03 ### 65 0.4 332 16 R46724 G-protein coupled hum 4.83e+03 ### 65 0.4 332 16 R46724 G-protein coupled hum 4.83e+03 ### 65 0.4 332 16 R46724 G-protein coupled hum 4.83e+03 ### 65 0.4 332 16 R32370 G-protein coupled hum 4.83e+03 ### 65 0.4 333 18 R32315 G-protein coupled hum 4.83e+03 ### 75 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 75 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 76 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 77 5 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 77 5 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 77 5 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 77 5 0.4 334 18 R32315 G-protein coupled hum 4.83e+03 ### 77 5 0.4 336 2 P70508 TrpD entirpe. 4.83e+03 ### 78 78 78 78 78 78 78 78 88 88 89 89 89 89 89 89 89 89 89 89 89	Mon Dec 21 09:28:26 1998 US-08-951-733-20.zeg	762 763 764 765 765 766 766 767 767 767 767 767 767	Mon Dec 21 09:28:26 1998 US-08-951-733-20.zeg
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5 0.4 681 8 843348 Siman GFAT.	915 5 0.4 475 3 P50544 Tabacco ribulose-high 438-03 916 5 0.4 482 3 R31469 Mann tissue PA varia 438-03 917 5 0.4 482 1 R70823 Raman tissue PA varia 438-03 918 5 0.4 482 1 R70823 Raman tissue PA varia 438-03 919 5 0.4 482 1 R70823 Raman tissue PA varia 438-03 910 5 0.4 482 1 R70823 Raman tissue PA varia 438-03 911 5 0.4 482 1 R70823 Raman tissue PA varia 438-03 912 5 0.4 501 8 R70923 Raman tissue PA varia 1438-03 913 5 0.4 501 8 R70923 Raman tissue PA varia 1638-03 914 5 0.4 527 1 R70823 RAMAN erythropostetin 638-03 915 5 0.4 527 1 R70823 RAMAN erythropostetin 638-03 916 5 0.4 527 1 R70823 RAMAN erythropostetin 638-03 917 5 0.4 527 1 R70823 RAMAN erythropostetin 638-03 918 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 919 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 919 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 910 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 911 8 70823 RAMAN erythropostetin 648-03 912 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 913 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 914 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 915 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 916 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 917 8 0.4 527 1 R70823 RAMAN erythropostetin 648-03 918 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 919 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 919 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 910 5 0.4 527 1 R70823 RAMAN erythropostetin 648-03 911 8 0.4 528 1 R50823 RAMAN erythropostetin 648-03 912 5 0.4 528 1 R50823 RAMAN erythropostetin 648-03 913 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 914 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 915 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 916 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 917 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 918 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 919 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 910 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 910 6 0.4 528 1 R50823 RAMAN erythropostetin 648-03 910 6 0.4 528 1 R50823 RAMAN	Mon Dec 21 09:28:26 1998 US-08-951-733-20.rag	### State	Man Dec 21 09:28:26 1998 US-08-951-733-20.zag

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	Page 23		Page 21
S Rome sapiens. Location/Qualifiers FT Propertie 117 FT protein 41.46 FT region 44.46 FT region 44.46 FT region 44.46 FT region 64.76 FT region 65.76 FT region 65.77 FT reg	Mon Dec 21 09:28:26 1998 US-08-951-733-20.zeg	Fit misc_difference inter- PT misc_difference inter- PT misc_difference inter- PT misc_difference incresponds to GAT codon' PT misc_difference incresponds to AGC codon' PT woologic. PN 10-728-1991 BEOOSIG. PN 10-728-1991 B	Non Dec 21 09:28:26 1998 US-08-951-733-20.rag

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Mon Dec 21 09:28:26 1998 US-08-951-733-20.rag
OS Human lymphotropic virus type II strain NRA-19a.
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21 09:28:26 1998

Page 26

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RESULT
AC WO
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10 STAN-193.

10 STAN-193.

11 STAN-193.

12 STAN-193.

12 STAN-193.

13 STAN-193.

14 (ABDO ) ABBOTT LAB.

15 Holey CT;

16 Guidinger P. Iller KB, Johnson JF, Lee HH, Moley CT;

17 Buytendorp HH, Chan FW, Chen ISY, Edwards M, Golde DW;

18 Buytendorp HH, Chan FW, Chen ISY, Edwards M, Golde DW;

19 Buytendorp HH, Chan FW, Chen ISY, Edwards M, Golde DW;

19 Buytendorp HH, Chan FW, Chen ISY, Edwards M, Hooley CT;

19 Feterson B, Robertson E, Rosenblatt JD, Stephens JE;

19 Stanson PA, Take C;

10 Restance CH, Take C, Rosenblatt JD, Stephens JE;

10 Restance CH, Stanson JC, Rosenblatt JD, Stephens JE;

11 Restance CH, Stanson JC, Rosenblatt JD, Stephens JC;

12 Restance CH, Stanson JC, Rosenblatt JD, Stephens JC;

13 Restance CH, Page 80 100pp; English,

14 Restance CH, Page 100 100pp; English,

15 Restance CH, Page 100 100pp; English,

16 Restance CH, Page 100 100pp; English,

17 Restance CH, Page 100 100pp; English,

18 Restance CH, Page 100 100pp; English,

19 Restance CH, Page 100 100pp; English,

10 C Overlap, and are involved in restrain processing, The Virus may be produced in cell culture ATCC

17 Restance CH, Page 100 100pp; English,

18 Restance CH, Page 100 100pp; English,

18 Restance CH, Page 100 100pp; English,

19 Restance CH, Page 100 100pp; English,

19 Restance CH, Page 100 100pp; English,

10 Restance CH, Page 100 100pp; English,

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12 Restance CH, Page 100 100pp; English,

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14 Restance CH, Page 100 100pp; English,

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19 Restance CH, Page 100 100pp; English,

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DE MASTAT Standard; Protein; 334 AA.

10 (1854); 184 (first entry)
20 (1800); 194 (first entry)
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pp 21-DEC-1995; US-76626.

pp 21-DEC-1995; US-76626.

pp 21-DEC-1995; US-76626.

pp 21-DEC-1995; US-76626.

pp 22-DEC-1995; US-7662
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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W03397; standard; Protein; 296 AA.
W03397; 19-PEB-1998 ((irst entry)
Ruman clone 55 protein.
Src-banelogy region 3 domain; human; mouse; 8H3 domain; cell growth; cellular signaling element; cellular structural element; malignancy; protein identification; functional domain; protein acreening; stano sapiens.
W00931635-A1.
W00931635-A1.
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251 SRSLPLP 257
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nathelmintic.
Saccharopolyspora erythraea.
209723630-A2.
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 11; Length 354; Pred. No. 4.52e+01; 0; Mismatches 0; Indels Recombinant interleukin-8 receptor polymeptide - having antinfiamatory properties
claim i, Figure 1, 13pp; Japanese.
Anti-inflamatory spone containing the interleukin-8 receptor polymeptide can be used for the treatment of peoriasis, rheumatoid arthritis and other coute and choronic inflamatory diseases, including reperfusion and allograft rejection.

Sequence 334 Ax;

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RESULT 6
ID M19716 standard; Protein; 333 AA.
ID W19716, 19716 standard; Protein; 333 AA.
AC 18-927-1997 (first entr)
DZ 80gar blooynthesis ensyme EnyBII; I-mycarose; antimicrobial;
EN Polyketide; glycosylation; eryBII; I-mycarose; antimicrobial;
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PF 03-APR-1996; U5-650915.

PR 07-APR-1996; U5-650915.

PR 07-APR-1996; U5-650915.

PR 07-APR-1996; U5-650915.

PR 07-APR-19978.

PR 10-APR-19979.

PR 10-BPR 10-BPR 10-BPR 10-BPR 10-BPR 10-BPR 19979.

PR 
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RO 5393; stundard; Protein; 354 AA.

RO 5393; (first entry)

DZ 13-FZE-1955 (first entry)

DZ 11-Ext-enkin 8 (II-8) receptor.

RW Interlenkin 8 (II-8) receptor; antiinflammatory; paoriasis; reperfusion;

RW Interlenkin; receptor; antiinflammatory; paoriasis; reperfusion;

RW Interlenkin; receptor; antiinflammatory; paoriasis; reperfusion;

RW Interlenkin; receptor; antiinflammatory broad;

DZ 12-PR-1995; 149245.

DZ 17-PR-1995; 149245.

DZ 17-PR-1995; 199146.

DZ 18-1991; 94-166556,19.

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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||||||||
304 atslega 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene - for production and engineering of myoinositol dehydrogenase Claim 3: Page 8-9: 13pp; Japanese. Claim 3: Page 8-9: 13pp; Japanese. The sequence (Q55708) shows a recombinant plasmid which encodes myoinositol dehydrogenase. The plasmid can be transformed into a suitable host thus producing myoinositol dehydrogenase quickly a suitable host thus producing myoinositol dehydrogenase quickly.
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|||||||
1141 ANPALPS 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 334 AA;
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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ID B
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December 12

RESULT 12

RESULT 12

RESULT 11: MAR-1997 (first entry)

DE Human Gyrokine response protein CB3.

RESULT 11: MAR-1997 (first entry)

RESULT 12: Annabuction

RESULT 13: Annabuction

RESULT 1
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12 (ALLE) B. LERGAN INC.

13 (ALLE) 98-1480, TW. Noodward DP:

14 (ALLE) 98-1480, TW.

15 (ALLE) 98-1480, TW.

15 (ALLE) 98-1480, TW.

17 (ALLE) 98-1480, TW.

18 (ALLE) 98-
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Best Local Similarity 100.0%;
Matches 7; Conservative
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241 pgarrrg 247
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RABET2: standard; Protein; 355 AA.
RABET2;
Od-APR-1993 (first entry)
Sequence in a high affinity recombinant rabbit interleukin-8
(II-8) receptor polypeptide in FBR.
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1104 LTRHRVT 1110
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Similarity 100.0%;
7; Conservative
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Pred. No. 4.52e+01;
0: Mismatches 0; Indels
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d. No. 4.52e+01;
Mismatches 0;
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                                                             in the detection and
the CR coding region
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ID #44346;

AC #44346;

DY 15-MAY-1998 (first entry)

DE Buman HP4 prostaglandin receptor;

KW Human; HP4 prostaglandin receptor; ac

KW GAMP.

OS Homo sapiens.

PM US5718835-A.

PM US571898; 239431.

PR 05-MAY-1998; 239431.
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98 00271034918 cunicitus.

99 00271034918 cunicitus.

99 10-20210392 cunicitus.

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes (see also 743376-8) isolated from a thiol-selected interlaukin 2-indused human T-cell blaat cDNA library. 6 Genes (CRL, 2, 3, 5, 6, 8) are novel. CR3 shows homology to 6-coupled 7 transmenbrane -panning receptors of the prostaglandin family and probably plays a regulatory role in cellular proliferation and/or inflammation. It provides a novel receptor that allows the manipulation of cellular functions controlled by blochemical pathways signalled by the receptor and may be used to identify lignals useful for medulating cellular proliferation and inflammation. Recombinant CR3 polypeptides can be produced in bost sequence 338 Ak.
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1104 LTRHRVT
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|241 PGARRRG
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Page 32 Score 7; DB 6; Length Pred. No. 4.52e+01; 0; Mismatches 0; Ir

Indels 355;

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251 247

Score Pred.

e 7; DB 20; Length . No. 4.52e+01; Mismatches 0; Inc

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RESULT 17
ID W24252 standard; Protein;
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PRO276. standard: Protein; 395 AA.

pro276. pro276. protein; 395 AA.

pro276. process of the stry)

E sequence encoded by $1 LVidans gal operon galk gene.

Sequence encoded by $1 LVidans gal operon galk gene.

Sequence encoded by $1 LVidans galo operon.

Streptomyces 11vidans strain 1226.

PR 20-ESP-1987; 970026.

PR 20-ESP-1987; 970026.

PR 20-ESP-1987; 970026.

PR 20-ESP-1987; 05-00419.

PR 20-ESP-1987; 05-00
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RECORD standard; Protein; 195 AA.

RECORD Standard; 195 A
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804 ETSPIRD 810
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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Pred. No. 4.52e+01
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RA1330 standard; Protein; 395 AA.

RA1330 standard; AA.

RA1330 standard; AA.

RA1330 standard; AA.

RA1330 standard; AA.

RA1340 standard; AA.

RA1340 standard; AA.

RA1350 st
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wordstander degenei etrain K4.

pp 14-NG-1997; U0104.

pp 21-JAN-1997; U0104.

pp 21-JAN-1996; US-59171.

pa (09-FES-1966; US-59171.

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     RESULT
ID R884
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DE Bete
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programmic library
ps Claim 31; Fig 5; 95pp; English.

Co This protein sequence comprises appartate aminotransferase KC/AA

Co This protein sequence comprises appartate aminotransferase KC/AA

Co Graws optimally at 70 deg C and pH 7.0 in low salt medium. The

Co claimed thermostable transaminases and aminotransferases (W4248-57)

Co Claimed thermostable transaminases and aminotransferases (W4248-57)

Co can be produced from native or recombinant host cells for use with

Co L- and/or D-amino acids for production of optically pure chiral

Co compounds used in the pharmaceutical, agricultural and other

Co industries. A method is claimed for transferring an amino dried to

Compounds used in the pharmaceutical, agricultural and other

Co industries and method is claimed for transferring an amino dried to

Compounds used in the pharmaceutical, agricultural and other

Co industries and anino acid to an alpha-beo acid using a claimed enzyme

Co industries an indicator of heart damage.
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     D 88807 standard; Protein; 429 AA.

R88407, (C 888407, (cfirst entry)

Betn-(1,8)-endoglucanase;
W Trichoderma harzianum beta-(1,8)-endoglucanase; As beta-glucan degradation; pustulanase.

S Trichoderma degradation; pustulanase.

M WD953133-AL.

21-807-1805.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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18 PEP-1908 (first entry)
18 PEP-1908 (first entry)
Ammonitex degensii appartate aminotransferase XC4/AA.
Aspartate aminotransferase; XC4/AA; chiral compound.
Ammonitex degensii strain XC4.
MD07129187-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                157 lraavtp 163
|||||||
437 LEAAVTP 443
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260 PRRGAAP 266
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N-SSD: GOODS.

Production of very long chain fatty acid(s) in plant(s) - to produce Production of very long chain fatty acid(s) in plant(s) - to produce drought and stress resistant transgenic plant(s) - to produce produce produce the produce produce to purification of jojobs and produce produce accurate acquence is application so 33/1024. Jojobs fatty acyl reduces acquence is hown. A membrane prepr. having wax synthase activity is isolated, the wax synthase activity is solabilised, and the sax synthase activity is solabilised, and the wax synthase activity in solabilised, and the wax synthase activity is solabil

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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 14; Length 493; Pred. No. 4.52e+01; 0; Mismatches 0; Indels

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PR 11-MA-1955; DROSS.

PR (1800) 18000-18000-1804.

PR (1800) 18000-1804.

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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 17; Length 429; Pred. No. 4.52e+01; 0; Mismatches 0; Indels 0 Caps

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RESULT 20

RESULT AC RANGE OF PR SOCIETY SELUT 19 877163 atandard: Protein: 493 AA. 877163 atandard: Protein: 493 AA. 877163 (Kirst entry) Jojoba fatty acyl reductase. very long chain fatty acid; acyl-coa; fat vax synthase. Jojoba. JOHN-1991; US-166602.
fatty acy1

HOB Dec 21 09:28:26 1998

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Indels 9

426 lllrlvd 432 |||||| 884 LLLRLVD 890

Length 493;

RESULT ID RI AC RI DT 11 LT 22 R26698 standard; Protein; 493 R26698; 15-PEB-1993 (first entry) Jojoba fatty acyl reductase.

US-08-951-733-20.

Length 493;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 18; Ler Pred. No. 4.52e+01; 0; Mismatches 0; Indels 0 Caps

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508 standard: Protein; 493 AA.
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joba fatty-acyl-reductase,
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pp 01-DMR-1995; 006670.
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Query Match
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R R SECOMAININI DM. comprises nucleic acid acquence which proceeding acquence incoding acquence with a construct in which the vax synthase gene is associated with a construct may be used to produce crop plants having a convenient course of vax setters. Wax esters can be used in a variety of construct may be used to produce crop plants having a convenient course of vax setters. Wax esters can be used in a variety of construct may be used to produce used in a variety of confidence in the construct may be used to produce used in a variety of confidence in the construct may be used to produce used in a variety of confidence in the construct may be used to produce used in a variety of confidence in the confidence in the construct may be used to produce used in a variety of confidence in the construct may be used to produce used in a variety of confidence in the confidence in the construct may be used to produce used in a variety of confidence in the construction of the confidence in 
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Dhachosure; Column 43-46; 30pp; English.

A jojoha fattyracyl-reductase ONN was used in the construction of vectors for plant transformation, Transgenic Plants, e.g. cliseed wax-synthase are used for wax ester prodn.

Sequence 433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 laslrps 517
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369 LSSLRPS 375
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                                                                                                                                                                                                                                                                                                                            517 AA;
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339..517
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels 0;
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Pred. No. 4.52e+01
0; Mismatches
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DESCRIPT 28

ID 970347;

AC 970347;

AC 970347;

DT 18-MAY-1991 (tiret entry)

DE Varicella-roster virus (VSV) immuno;

RW Varicella-roster virus; gB gene proc

RW Varicella-roster virus; gB gene proc

RW 12-702-1987;

PD 12-70
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2 12-ARR-1990.

3 16-OCT-1998: J0-249922.

3 05-OCT-1998: J0-249922.

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3 05-OCT-1998: J0-249922.

3 16-OCT-1998: J0-249922.

3 17-OCT-1998: J0-249922.

4 17-OCT-1998: J0-249922.

4 17-OCT-1998: J0-249922.

4 17-OCT-1998: J0-24992.

5 18-OCT-1998: J0-24992.

6 18-OCT-1998: J0-24992.

7 18-OCT-1998: J0-2492.

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7 18-OCT-1998: J0-2492.

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pp 01-7UN-1996: U05-251464.
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pp 141: 96-010586/03.
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Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 mrplfle 607
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411 MRPLFLE 417
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|||||||
884 LLLRLVD 890
                                                                                      Prayment of varicella-soster virus - used for producing poly:peptide for use as vaccine against VEV disease and pox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             970347;
18-MAY-1991 (first entry)
Varicella-zoster virus (VSV) immunogenic outer surface protein.
Varicella-zoster virus; gB gene product; varicelka; vaccine.
EP-310931-A.
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Resynthesised jojobs (atty-acyl-reductase,
Sojobs, fatty-acyl-reductase, enzyme, transgenic plant,
Claim 2; Page 25-28; 29pp; English.
The protein sequence encodes an immunogenic
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-1-6-glucanase.
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roides thetaiotamicron K
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KHM098.
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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      outer surface VZV protein
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is useful for the
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pTG1200; oxaloacetate;

O'Reagan

Score 7; DB 4; Leng Pred. No. 4.52e+01; 0; Mismatches 0;

Length 868;

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RESULT 39

RESULT 393 (first entry)

RESULT 394 (first entry)

RESULT 394 (first entry)

RESULT 394 (first entry)

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pp 01-MR-1997; 004577.

pp 04-MR-1996; 03-0073117.

pp 14-MR-1996; US-01346.

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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                      NULT 12 W27084 tandard: Protein: 946 AA. W27084.
18 -MAR-1998 (first entry)
Ruman cytomegalovirus (ECMY) UL70 tz
Ruman cytomegalovirus hallcase; ECMA
infection; diagnosis; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
Homo sapiers. and Market GB3111068-A.
17-SEP-1997; 004575.
05-MAR-1997; 004575.
04-ARR-1996; GB-007118.
14-KAR-1996; GB-007118.
14-KAR-1996; GB-007118.
05-11b L. Hasuda DJ, Lafemina R.
WPI: 97-487906/40.
P-PSDB; W27083.
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disease, varicella. 7
VZV antibody titers.
Sequence 854 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 slrtagt 403
||||||||
1117 SLRTAQT 1123
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Ruman cytomegalovitus (ECMV) primase.
Human cytomegalovitus primase; HCMV, acreening; inhibitor; infection; disposis; da.
Homo espiers.
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894 LVTPHLT 900
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The antigen
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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Pred. No. 4.52e+01;
0; Mismatches 0; In
                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                  70 translation product HCMV UL70; screening;
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is also used
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ROSSLIZ standard: protein: 91

ROSSLIZ standard: protein: 92

ROSSLIZ standard: 92

ROSSLIZ standard: 93

ROSSLIZ standard:
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21-MAR-1989: 114632: 9
21-SEP-1989: 68-031119.
21-SEP-1989: 68-031119.
21-SEP-1989: 68-031119.
21-SEP-1989: 68-031119.
21-SEP-1989: 68-031119.
21-SEP-1989: 68-03119.
21-SEP
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ID W27085 standard; Protein;
AC W27085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ec
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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|||||||
621 RELSEAE 627
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Sequence 868 MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 lytphit 293
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894 LYTPHLT 900
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Phosphoenolpyruvate carboxylase;
Phosphoenolpyruvate carboxylase;
Corynebacterium glutamicum.
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THE RESERVE TO SOLUTION OF THE PROPERTY OF THE

946

Score 7; DB 1; Length 919; Pred. No. 4.52e+01; 0; Mismatches 0; Indels

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the anaplerotic function of the cell-it indirectly increases biosynthetic

for

pr Novel human cytomegalovirus helicase . used for screening for RCMV PT antivirals and in diapposis of IRMV related diseases 98 Example 1; Pages 20-21; Pagp; English.

CC The present sequence represents human cytomegalovirus (RCMV) UL70 ct ansiation product. The UL70 open reading frame spans nucleotides co 19505-6. The amplified product was disperted with Rel and XmaI and CC cloned Ainto Net/Lord disperted 1987786 vector DNA to yield the plasmid product were determined. Recombination into BacPAK of viral DNA, plaquel CC product were determined. Recombination into BacPAK of viral DNA, plaquel CC purification and generation of viral stocks were by standard protocols. The protect was used with a new ENGW helicase in a screening stock of compounds which inhibit BMCV helicase (prefetably with an IC50 CR result greater Hum 200Ms), and as a diagnostic tool for diseases so sequence 940 AM. Intection.

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 26; Ler Pred. No. 4.52e+01; 0; Mismatches 0; Length 946; 0

Gaps

0

397 slrtagt 403 ||||||| 1117 slrtagt 1123

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RESULT. 33

AC R76005; standard; Protein; 966 AA.

AC R76005; defect; alterativ)

DY 16-7Mx.1996 (first entry)

DY cast MSD2 protein.

RW Alsanch repair; MSD2; primer; identification; defect; alteration;

RW Alsanch repair; MSD2; primer;

RW MSD3,4083-A2.

OS Succharouses cerevisiae.

PW N09514083-A2.

OS Succharouses cerevisiae.

PW N09514083-A2.

DY 18-MX 193; U3.18479.

PD 23-MX 193; U3.18479.

PD 23-MX 193; U3.18479.

PD 21-MX 193; U3.18479.

PD 11-MX 193; U3.18479.

PR 11-UNN.193; U3.18479.

PR 11-UNN.

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No settephococcus salivarius strain ANCC 25973.

BN 4050613134.

PR 143C-1959: AUGS27.

PR 24-10C-1959: AUGS28.

PR 24-10
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RETURN

                                                                                                                                                                        Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
      1174 rrvgddv 1180
|||||||
| 164 RRVGDDV 170
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|||||||
523 aklsigz 529
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pha-D-glucosyltransferase,
pha-D-glucosyltransferase,
pha-D-glucosyltransferase,
primer-independent, soluble glucan;
person plant, cloning, Escherichia colliscoso;
seg lambda-cl), vectory plannid poscoso;
seg lambda-cl), vectory plannid poscoso;
seg lambda-cl), vectory plannid poscoso;
plannid poscoso;
sed trusti; secosoc; sextran binorage carbohydrate; parture;
redsruft; secosoc; sextran binorage (2004) pharmaceutical.
redsruft; secosoc; sextran binorage (2004) pharmaceutical.
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Pred. No. 4.52e+01;
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15
10 1930
16 standard; Protein; 1539 AA.
16 10 1970; 1977 (first entry)
17 10 1970; 1977 (first entry)
18 Human Short protein
18 Short; rotein
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AC RS
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pp 14 - SEP 1995; U3 - 003744.

pp 14 - SEP 1995; U3 - 003744.

pp 17 - NAR 1995; U3 - 003744.

pp 17 - NAR 1995; U3 - 003744.

pp 17 - NAR 1995; U3 - 00374.

pp 18 - 00374.

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Stription of the property of the prope
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
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||||||||
1079 GAKGAAG 1085
17 38
R95119 standard; peptide; 7 AA.
R95119 standard; peptide; 7 AA.
18-DEC-1996 (first entr)
19-DEC-1996 (stirst entr)
Peptide provides site for much sugar chain introduction
clycosylation site; much sugar. N-acety; galactosamine;
berspeutic polypeptide; erythropoietin; interferon.
N99613516-A1.
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Sequence 1366
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sinc finger 7 randomised residues with affinity for HIV-
is sinc finger 7 randomised; alpha-helical region; slif268;
linger; variant; randomised; alpha-helical region; slif268;
limminodeficiency virus; cherapy tirus infection;
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ription-activator; transcription-inhibitor; plant disease
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Pred. No. 4.52e+01
0; Mismatches
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Pred. No. 4.52e+01;
0; Mismatches 0; Indels
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1: £1f268;
HIV-1;
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RESULT 39

RESULT 39

REAL 43371 etandard: peptide: 10 AA.

AC 443371 peride: peptide: 10 AA.

DE J. A. 1999 (first entry)

DE J. A. 1999 (first entry)

DE J. A. 1999 (first entry)

REAL 4371 etandard: peptide derived from HBc 18-27.

REAL 1997 movif; HA.-A. 1 allels: immunogenic peptide; cancer;

REAL 1997 movif; HA.-A. 1 allels: immunogenic peptide; cancer;

REAL 1997 movif; HA.-A. 1 allels: immunogenic peptide; cancer;

REAL 1997 movif; HA.-A. 1 allels: immunogenic peptide; cancer;

REAL 1997 movif; HA.-A. 1 allels: immunogenic peptide; cancer;

REAL 1997 movif; BC.

PER 1997 movif; M. 1998 movif; Per 1 allels: immunogenic peptide; peptide;

PER 1997 movif; M. 1998 movi
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pp 01-RWY-1995, J09218.

pp 01-RWY-1995, JP-252111.

pp 02-RWY-1995, JP-25211.

pp 12-RWY-1995, JP
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1117 SLRTAG 112
NO9703358-A1. /note* 'Phosphotyrosine'
30-JM-1397; 01-206.
07-JU-1395; 01-206.
07-JU-1395; 05-00971.
(USSH ) US DEPT ERLITE & HOMAN SERVICES.
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Query Match 0.5%; Best Local Similarity 100.0%; Matches 6; Conservative Agents which inhibit the Jak-Stat signal transduction pathway were identified in order to identify candidate drugs for treatment of profits active disorders and transplant rejection. Schools of its the identification were based on inhibiting the interestion of its) the activated stat search profits transcription in the State seat profits and profits profits on the State seat profits are profits profits on the State seat and seat profits and profits profits on the State seat and seat profits and profits and profits and the state seat of the state re 6; DB 23; Leng d. No. 5.54e+02; Mismatches 0; Length 12

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RESULT 42

DR 593465 standard; peptide; 14 AA.

DR 593465, 29366 (first entry)

CR 593467, 29366 (first entry)

REF 1936, 29366 (first entry)

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10 High standard; peptide; 15 AA.

11 High standard; peptide; 15 AA.

12 High standard; peptide; 15 AA.

13 High standard; peptide; period; pe
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pp 23-MRR-1997; 004176.

pp 21-MRR-1996; US-622338.

pp 22-MRR-1996; US-622338.

pp 22-MRR-1996; US-622338.

pp 22-MRR-1996; US-622338.

pp 22-MRR-1996; US-622338.

pp 23-MRR-1996; US-622338.

pp 24-MRR-1996; US-622338.

pp 24-MRR-1996; US-62338.

pp 24-MRR-1
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Tannactivating protein; Tax; peptide fragment #36;

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67 AAFRAL 72
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0; 1
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                   re 6; DB 11; I
d. No. 5.54e+02;
Mismatches C
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host cell; transcription;
regulation;
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Score 6; DB 26; Len Pred. No. 5.54e+02; 0; Mismatches 0;

Length 16; Indels

0

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Query Match 0.5%; Best Local Similarity 100.0%; Matches 6; Conservative Score 6; DB 28; Length 20; Pred. No. 5.54e+02; 0; Mismatches 0; Indels 0

IESUL7 50

DE 874374 standard; peptide; 20 AA.

C 574374, 1996 (first entry)

T 31-3AM-1996 (first entry)

MY Human F-cell lymphotropic virus type 1; HTV-1; P40(tax) provider antigence peptide; TATO; residues 265-305; adult T-cell levi to antigence peptide; TATO; residues 265-305; adult T-cell levi to antigence peptide; TATO; residues 265-305; adult T-cell levi to HTV-1; associated myclopathy.

MY HUMAN lymphotropic virus type 1.

MY US-420244-A.

PO 30-MY-1993; 103742.

PR 06-AUG-1993; 103742.

PR 06-AUG-1993; US-03742.

PA (USSH) US DEPT HEALTH 6 HUMAN SERVICES.

protein; leukaemia;

RESULT
ID R7AC
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Dec

13 MAY-1998 (first entry)

Tax protein frequent;
Tax dependent transcription;
Tax-dependent transcription;
Viral infection;
Jaments disorder;
Longrygous familial hypercholesterolaemia;
Longrygous familia hypercholesterolaemia;
Longrygous familia hypercholesterolaemia;
Longrygous familia hypercholesterolaemia;
Longrygous fa

Gaps

12 psf11s 17 | | | | | | | | 365 PSFLLS 370

10 - FEE - 1994; 199508.

10 - FEE - 1994; 199508.

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15 - FEE - 1994; 199508.

16 - FEE - 1994; 199508.

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17 - FEE - 1994; 199508.

18 - FEE - 1994; 199508.

18 - FEE - 1994; 199508.

19 - FEE - 1994; 199408.

19 - FEE - 1994; 1

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Page 63

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for diagnosing HTLV-I myelopathy and adult T-cell

r g f f f g g g g g g g g

Lal BB. Rudolph DL/
WPI. 95-20630727.
WPI. 95-20630727.
Rev HTM-I anxignto peptide(s) - used for disgnosing HTM-I
intection(s), partic. HTM-I associated myslopathy and adult T-cel
leukemic.
Example 1.
Columns 11-12; 21pp. English.
274356-274375 are human T-cell lymphotropic virus type I (HTM-I)
p40(rax) protein antigent peptides. They can be used to disgnose
diseases assed by HLTM-I, e.g. adult T-cell leukaemia, and HTM-I
sequence 20 Ah;

Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative Score 6; DB 14; Ler Pred. No. 5.54e+02; 0; Mismatches 0; Length 20; 0 Caps

9

Ş 밁 3 psflis 8 ||||||| 365 PSFLLS 370

Search completed: Fri Dec Job time : 183 secs. 18 19:07:44 Page 61

Mon Dec 21 09:28:26 1998

US-08-951-733-20.rag

Page 62

333 SRPPRP 338

DT 27-3N1-998 (first entry)
DE Beta-92-crystallin fragment (amino acida 85-101).

KW peta-19-crystallin fragment (amino acida 85-101).

KW epithelial cell; epitope.
OS Synthetio.
OS Homo aspians.
PN EP-70398-A2.
PO 10-0X1-3997.
PO 10-0X1-

wir. \$7'-237935/22.

In wish are containing less antigen or microorganism that expresses proceed to treat or prevent catanate by reducing the level of prantibodies directed sgafant less protein

Example 4; Page 29; Jäpp: English.

Comissequence is an internal fragment of human beta-92-crystallin. Comissequence is an internal fragment of human beta-92-crystallin. Comissequence is an internal fragment of human beta-92-crystallin and crespective olispoppides. As a result, only spetide fragment amino combeta-92-crystallin. This suggests that the binding site (spltope) of the 92-crystallin. This suggests that the binding site (spltope) of the 92-crystallin or the antional was a result in the second process of the second process of an antigens of sequence of anino acids numbers 162-165 of beta-92-crystallin or a nicroorganism hat can express a less antigens are used on a pharmaceutical composition. The composition can be used to prepare can inhibitor of an incress of anti-lens procein antisodies. The composition can be used to prepare composition that the binding of the pharmaceutical composition and the composition of the

Query Match 0.5%; Best Local Similarity 100.0%; Matches 6; Conservative Score 6; DB 25; Length 17; Pred. No. 5.54e+02; 0; Mismatches 0; Indels 0 Gaps 0

10 lsslrp 15 ||||||| 369 LSSLRP 374

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Ş RESULT 49
ID W41212 standard; peptide;
AC W41212;

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ENTRY ENTRY ENTRY A2834 stype complete 7171.E Procein tyrasine phosphatase (EC 3.1.3.48) Ly-5 precursor ALTERNATE, NAMES 200K Lenkovyre common antigen; CD45; PPFFT1; T-cell surface COPTAINS CORNISH FORMAL DAMES 100K Lenkovyre common antigen; CD45; PPFFT1; T-cell surface P1 yourpopterin Ly-7200ksse (T-cell veriant) CORANISH FORMAL DAMES 100K Lenkovyre common antigen; CD45; PPFFT1; T-cell surface P2 ybar-1998 sequence_prision 10 ybay 1889 sext. A8334 AL1; Reynolds, P.J.; Chain, A.; Ben-Neriah, T.; FORMAL PROCESSIONS A8334 AL1; Reynolds, P.J.; Chain, A.; Ben-Neriah, T.; FORMAL PROCESSIONS A8334 AL1; Reynolds, P.J.; Chain, A.; Ben-Neriah, T.; FORMAL PROCESSIONS A8334 AL1; Reynolds, P.J.; Chain, A.; Ben-Neriah, T.; FORMAL PROCESSIONS A8334 AL1; Reynolds, P.J.; Chain, A.; Ben-Neriah, T.; FORMAL PROCESSIONS A8334 AL1, PROCESSIONS A8334 AL1, PROCESSIONS A8334 AL1, Acad Sci. U.S.A. (1997) 84:5160-516 FORMAL PROCESSIONS A8334 PROCE	Man Dec 21 09:28:27 1998 US-08-951-733-20.xpx	971 6 0.5 2142 2 B35998 NRC class III histoco 5.47+402 973 6 0.5 2279 1 CORPRIA 974 6 0.5 2271 6 SATEMAN 975 6 0.5 2271 1 SANYAM 975 6 0.5 2271 1 SANYAM 975 6 0.5 2272 1 GANYAM 975 6 0.5 2272 1 GANY	Mon Dec 21 09:28:27 1996 US-08-951-733-20.TPX
	Page 23		Page 21
**crossion A6933 **crossion A6933 **prolecula_Type purple. **prolecula_	Mon Dec 21 09;28;27 1998 US-08-951-733-20.zpz	CLASIFICATION *superfamily leukocyte common antigen; protein; tyrosine; phosphatase homology leveryship protein; tyrosine; phosphatase homology leveryship protein; leukocyte common antigen; leukocyte common levek; leukocyte common antigen; leukocyte common leukocyte leukocyte common antigen; leukocyte common leukocyte le	Hon Dec 21 09:28:27 1998 US-08-951-733-20.zpz

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Coyte common antigen, 200% sstatus
LubelN937
... yte common antigen; leukocyte common; domain homology;
phosphatase homology
g; djycoprotein; phosphoric monoester
e antigen; transmembrane protein;
phosphatase er, C.M.; Pingel, J.T.; Thomas, M.L. 39) 264-6220-6229 Ion in potential regulatory regions of the leukocyte common antigen gene. Shen, F.W.; Boyse, E.A. Sci. U.S.A. (1987) 84:5364-5368 S' exons in the specification of Ly-5 ishing hematopoietic cell lineages. 8) 28:271-277 of Ly-5 glycoproteins of the mouse and other mammals. OH NID:g198755; PID:g554185; GB:J04640; ore 9; DB 2; Length 183; nd. No. 1.20e-03; Mismatches 0; Indels 0; Gaps 0; aggent
tigen precursor - mouse (fragment)
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od. No. 1.20e-03;
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Page 24

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Page 25

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Page 26

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ACCESSIONS

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RPPERENCE

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RPPERENCE

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A274
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Best Local Similarity 100.0%; Pred, No. 1.64e-01;
Matches 8; Conservative 0; Nismatches 0; Indels 0;
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sjournal PEBS Lett. (1986) 209:219-222
stitle Expression cloning of a cDM, encoding the type II regulatory ecross-references MUTI:57080763
sccession A3552.
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Best Local Similarity 100.0%; Pred. No. 1.20e-03;
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#Gross-references EMBL:X04370; NID:g59989; PID:g60048
                                                                                                                                                                                Pichl, J. Stocking, C.; Stocey, A.; Ostertag, W.
J. Vichl. (1987) 6:1889, gencey, A.; Ostertag, W.
J. Vichl. (1987) 6:1889, gence of the mysloproliferative
acroma virus, altered mysloprolime meation in the mos
oncogne, has been modified as a selectable retroviral
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*accession A1477

*spolecula Lye protein

*sresidues A1570

*strate A15740

*REFERENCE Kellwoge, A.R.; Taylor, S.S.

*journal J. Blol. Chem. (1980) 325-884

*title Covalent modification of an a
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Best Local Similarity 100.0%; Pred. No. 1.64e-01; Indels
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 164e-01;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps
                    *cross-references MUID:8100688
*accession A15740
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461 EEEDTDPR 468
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protein kinnas (CC 2.7.1.37), cAMP-dependent, type II-alpha
regulatory chain - bowlin
stormal_name Bos prindgenius carrus scommon_name cattle
15-oct-1992 sequence_revision 15-oct-1992 stext_change
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A00518; $17058
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Tablo, R.; Smith, S.B.; Krebs, E.G.; Walsh, K.A.; Titani, K.
Tablo, R.; Smith, S.B.; Krebs, E.G.; Walsh, K.A.; Titani, K.
Tablo, E.G.; Walsh, C.S.; Thosphate dependent protein
tipsemostie cyclic 3.7.° phosphate dependent protein
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J. Biol. Chem. (1980) 255:8483-8488
Govalent modification of an adenosine J'.5'-monophosphate-
binding site of the regulatory subunit of CAMP-dependent
projects kinase II with 9-asidoadenosine
3'.5'-monophosphate.
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Fregion protein kinase ATP-binding motif\
#active_site Lys #status predicted
#length 342 #molecular-weight 37970 #checksum 8888
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Kinase homology
ATP; oncogene; phosphotransferase; serine/threonine-specific protein kinase; transforming protein
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domain homology (frequent) #label CAP
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Db 8 LAPGFALLD 16 [[]]|||||| Oy 119 LAPGFALLD 127

SUMMARY

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587-1291 64,150,161,207,211, 218,253,258,290, 311,322,347,416, 427,457,489,520,

ACCESSIONS REFERENCE #authors #journal #title

egene CLASSIFICATION KEYWORDS

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COMMENT

chains and two catalytic chains. Activation by cAMP produces two active catalytic monomers and a regulatory dimer that binds four CAMP molecules.

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COMMENT COMMENT oby molecules.

Four types of regulatory chains are found: I alpha, I beta, II alpha, and II beta. Their expression varies among tissues and is in some cases constitutive and in others inducible.

Type II regulatory chains are phosphorylated by the activated catalytic chain. The physiological significance of phosphorylations by other Kinsses as molecularities that the phosphorylation by an accomplished the phosphorylation of the pho

CLASSIFICATION esuperfamily cAMP-dependent protein kinase regulatory chain; cAMP receptor protein cyclic nucleotide-binding domain

KEYWORDS nomology acetylated amino end; cAMP binding; duplication; heterotetramer; homodimer; phosphoprotein;

PEATURE 1-134 135-256 -257-389 demain protein interaction slakel DIN domain oMMP receptor potein cyclic nucleotide-binding domain homology slabel CAL cyclic nucleotide-binding domain homology slabel CAL cyclic nucleotide-binding domain homology slabel CAL cyclic and slate acceptance of the cyclic acce

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Db 106 EEEDTDPR 113
Qy 461 EEEDTDPR 468

OKHUJA: «type complete
protein kinase (52 27.1.37), cAMP-dependent, type II-alpha
regulatory chain - human
sformal_name Emmo sapiene scommon_name man
1:Mar-1993 seequence_revision 31-Mar-1993 stext_change
02-Sep-1997

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#length 404 #molecular-weight 45518 #checksum 9820

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 404; Pred. No. 1.64e-01; 0; Mismatches 0; Indels 0; Gaps

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ACCESSIONS REFERENCE *authors *journal *title Nonura, O.; Rakabayashi, O.; Rishimori, K.; Misuno, S. Gene (1997) 165:317-222
The oDNA cloning and transient expression of a chicken gene encoding cytechrome P-450sec.
Adrenal gland
UC\$200

*accession

AGENCE AGENCATION REPRODES PENTURE 452 pescal *superfamily cytochrome P450 heme; steroid binding

SUMMARY ebinding_site heme iron (Gys) (axial ligand) estatus
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elength 508 smolecular-weight 50195 echecksum 7347

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ALTERNATE_NAMES 10 HRBYS1 stype complete dnak-type molecular chaperone SSC1 precursor, mitochondrial yeast (Saccharomyees cetrevisiae) productions of the chain; endonuclease Scel JSK chain; endonuclease Scel large chain;

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GCTGSTeferences EMDS::M2722; NID:g341653; PID:g717089
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**S1116*

**Nuthors Morishma, N.; Nakagawa, K.; Yamamoto, Z.; Shibata, T.
**Journal J. Biol. Chem. (1990) 265:31319-31317

**Ittle A submit of yeast site-specific endouclease SceI is a
**microhondrial version of the 70-kDa heat shock protein.
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***molecule_type 10-643, 'Nr. 564-649, 'Dr. 551-554 **slabel MOR

***redicted chemical 50:155277; G3:J05574; MD:9171462; PID:9171463

**molecule_type protein

**molecule_type protein

molecule_type 2-41*eslabel MOR2

molecule_type 3-41*eslabel MOR2

**specific service Schemer 0 **slabel MOR2

**specific service 0 **slabel MOR

REFERENCE #authors #journal Scherer, P.B.; Krieg, U.C.; Bwang, S.T.; Vestweber, D.; Schere, G. Bobo J. (1990) 9:4315-4322 Porcutsor protein partly translocated into yeast mitochondria is bound to a 70 kM mitochondrial, tress

-cin parity
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brission substred to the Protein Sequence Database, September 1995
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SO1885 SO1985 Oeyen, O.; Myklebust, F.; Scott, J.D.; Hansson, V.; Jahnsen,

PEBS Latt. (1989) 246:57-64

Ruman tests cDNA for the regulatory subunit RII-alpha of CAMP-dependent protein kinase encodes an alternate amino-terminal region.

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FEATURE 2-404 ogy ted amino end; cAMP binding; duplication; otetramer; homodimer; phosphoprotein;

2-138 139-260 261-393 sproduct protein kinase, oMp dependent, type II-alpha regulatory ohin setation predicted \$label MNT.

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##cross-references SGD:S0001445; MIPS:YIR006c
#map_position 9R
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Nucleotide acquence and analysis of the centromeric region of year chromosome IX.
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uurr Genet. (1991) 19:495-502
Homology between mitochondrial DNA of Agaricus bisporus and
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YQKKRK', 'KGHNQFLLQVSHQFHLQVFLHPHPHPHEDLICFL' ##1abel
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Best Local Similarity 100.0%; Pred. No. 164e-01;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Query Match 0.6%; Score 7; DB 2; Length 23;
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Matches 7; Conservative 0; Mismatches 0; Indels 0;
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**accession JR0515

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The Lowe's couldocarbhoranal syndrome gene encodes a protein highly homologous to inositol polyphosphate-5-phosphatesenoids
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Blochem, Blophys. Res. Commun. (1991) 181:1131-1136
Blochem, Blophys. Res. Commun. (1991) 181:1131-1136
Identification and NB3-terminal amino acid sequence of three
insulin-like growth factor-binding proteins in porcine
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Query Match 0.68; Score 7; DB 2; Length 52; Best Local Similarity 100.08; Pred: No. 1.32e+0; Matches 7; Conservative 0; Hismatches 0; Indels

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RESULT 16
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Fortin, M.; Barton, A. B.; Kabacy, D. B.; Claby,
Saubmission submitted to the EMB1 Data Library, Pebruary 1994.

**Rescription Sequencing of Chromosome I of Seccharomyces carevisiae:

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Thyrottopin receptor measenger ribonucleic acid is expressed stitle. Thyrottopin receptor measenger ribonucleic acid is expressed in most brown and white adipose tissues in the guines pig. seroes references MUID:92191878

**Accession A4918**

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Nucleotide sequence of Hansenula polymorpha DNA region
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Krutilina, A.I.; Seregina, S.A.; Tikhomirova, L.P.; Kryukov,
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rjournal pron Natl. Modyred, E.A. (1985) 82:7360-7363

rcoss-reference MUID. 860/2665

rcoss-reference MUID. 800/266

rcoss-reference MUID. 810/2669

reference MUID. 81
         ORGANISM
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ENTRY
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Best Local Similarity 100 0%; Pred. No. 1.32e-01;
Matches 7; Conservative 0; Mismatches 0; Indels
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99 LKELVAR 105
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myosin catalytic light chain, ventricular and slow striated
muscle - nouse (fragment)
myosin akali light chain
fformal_name has musculus focumon_name house mouse
10.-me-1989 sacquence_revision 01-bec-1889 ftext_change
01-u---1989 sacquence_revision 01-bec-1889 ftext_change
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hypothetical protein YHR212c - yeast (Saccharomyces
hypothetical protein YHR212c - yeast (Saccharomyces
formal_name Saccharomyces cerevisiae
02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change
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Ly-5-8 glycopyctein - mouse (fragment)
Fformal_name Mus musculus #common_name house mouse
05-Jun-1987 sacquence_revision 05-Jun-1987 stext_change
20-Mar-1998
         877068 stype complete
hypothetical protein - Synechocystis sp. (PCC 6803)
sformal_name Synechocystis sp.
pcc 6803
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Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.Z.
Si.; Buckingham, M.Z.
Ruclaid, Acids Res. (1989) 16:10037-10052
Promoter analysis of myosin alkali 19th chain genes
expressed in mouse striated muscle.
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Pred. No. 1.32e+01;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.32e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
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**Crosa-references MUID: 97061001 regions.

**Status Prilminary Status Prilminary Prilminary Status Prilminary Prilm
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||||||
811 AVVIEQS 817
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7-cell receptor alpha chain precursor V region (CTL-L17)
humal name Homo sapiens scommon_name man
17-Mar-1987 sequence_revision 17-Mar-1987 stext_change
02-Sep-1997
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8770cs 82770cs 827
Leiden, J.H.; Fraser, J.D.; Strominger, J.L.
Immunogenetics (1986) 41:17-23
The complete primary structure of the T-cell receptor genes
from an allored cytotoxic human T-lymphocyte clone.
ices MUID:86376770
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Bakamuta, Y. Hiyajiam, N.; Hitosawa, M.; Sujiura, M.;
Samamoto, S.; Kimura, T.; Hosuonchi, T.; Matsuno, A.;
Muraki, A.; Makasaki, N.; Matsuo, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Mada, T.; Matsunba, A.; Kamada, M.;
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*cross-references MU *accession A02016

RESULT 24 ENTRY TITLE Db 58 LRPSLTG 64 |||||||| Oy 372 LRPSLTG 378 Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 2; Length 148; Pred. No. 1.32e+01; 0; Mismatches 0; Indels 0; Gaps

ACCESSIONS
REFERENCE
*authors
*submission
*accession SEATRY 864794 stype complete
TITLE hypothetical protein YLL042c yeast (Saccharomyces
hypothetical protein LO737
ORGANISH STORMAL_name Saccharomyces cerevisiae
DATE 01-Ng-1995 sequence_fevision 14-May-1996 stext_change
14-Ng-1997

FURDAMEN

***CHARGE NOTE: H.: Wedler, E.: Scharfe, K.: Wambutt, R.

***Unition wider, H.: Wedler, E.: Scharfe, K.: Wambutt, R.

***Charge of the Protein Sequence Database, May 1996

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Qy 882 DGLLLRL 888 Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative 36 DGLLLRL 42 Score 7; DB 2; Length 167; Pred. No. 1.32e+01; 0; Hismatches 0; Indels 0; Gaps 0

ORGANISM DATE RESULT 25 ENTRY TITLE ACCESSIONS REFERENCE *author* Rakihara, Y.; Reimann, J.; Michalopoulos, E.; Ciccone, E.; Moretta, L.; Mak, T.W.

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Dec 21 09:28:27 1998 US-08-951-733-20.rpr

FEATURE
1-26
27-169 #journal J. Exp. Red. (1989) 169:393-405
#ititle Diversity and structure of human Tell receptor delta chain
genes in peripheral blood gamma/delta-bearing T
#cross-reference MUID:8999429
#accession 504915
#accession 504916
#accession 504916
#accession 1:168 #inbel TAX
#arceiduces 1:168 #inbel TAX
#arceiduces translation of the nucleotide sequence is not complete
#ASSITICATION #auperfamily immunoglobulin V region; immunoglobulin homology
#YFORDS
T-cell receptor

27-118 134-148 150-168 SUMMARY Quary Match 0.6%; Score 7; DB 2; Length 168; Best Local Similarity 100.0%; Pred. No. 1.32+01; Matches 7; Conservative 0; Mismatches 0; Indels 0 Gape 0

RESULT 26
ENTRY
TITLE
ORGANISM
DATE Db 4 LLGASVL 10 ||||||| Qy 697 LLGASVL 703

ACCESSIONS REPERENCE *author* *journal *title *accession. UC5478
*archidect. Type DBA.
**Inchest. 2054/8
2054/6
Hishida, T.; Ivasaki, H.; Ishioka, K.; Shinagawa, H.
Gene (1995) 192:63-70
Rolecular analysis of the Pseudomonas scruginosa genes, ruvk,
ruvB and rurc, involved in processing of homologous
recombination intermediates.

Page 41

Mon Dec 21 09:28:27 1998

Page 42

This sequence was derived from a human cytotoxic T-lymphocyte that is T3+, T4+, T8-.

egene GDB:TCRA

approserre GDB:120404; ONIX:186880

anp_position 14q11.2-14q11.2

classification equercianily immunoglobulin v reEXTWORDS slycoprotein; heterottramer; rePRATURE slycoprotein; betweettramer; rePRATURE slycoprotein; betweettramer; re127 eproduct T-cell receptor all eupperfamily immunoglobulin V region: immunoglobulin homology
glycoprotein; heterotetramer; receptor; T-cell

SUMMARY 28-120 121-125 126-139 49-116 93 predicted predicted employers 15441 echecksum

Ouery Match 0.6%; Score 7; DB 1; Length 139; Best Local Similarity 100.0%; Pred. No. 1.32e+01; thatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 4 LLGASVL 10 ||||||| Oy 697 LLGASVL 703

RESULT 23
ENTRY
TITLE
ORGANISM
DATE \$30280 ftype complete
hpcR protein Excharichia coli
formal_name Excharichia coli
10-Sep-1993 esequence_revision 30-Sep-1993 ftext_change
09-Sep-1997

ACCESSIONS REFERENCE fauthors fjournal ftitle siologie Roper, D.I.; Favrett, T.; Cooper, R.A. Mol. Gen. (1993) 237:241-250 The Bacherichia coli C homoprotecontechnate degradative operon: he gene order, direction of transcription and control of expression.

#accession 53020 #molecut_type DNA ##residues_type 1-148 ##1abel ROP #across-references GB:555952; NID:9298654; PID:9298655

hpeR
DNA binding: transcription regulation
elength 148 #molecular-weight 17255 #checksum 5904

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SUMMARY

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eproduct endodeoxyribonuclease ruvc estatus predicted elabel M7 elength 174 emolecular-weight 18556 echecksum 8754

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Best Load Similarity 100.0%; Pred. No. 1.32e-01; Macches 7; Conservative 0; Mimmaches 0; Indels 0; Gaps
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Best Local Similarity 100.0%; Pred No. 132+01; Indels 0; Gaps
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
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242 GARREGG 248
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|||||||
856 GSILSTL 862
                                                                                                                                                                                        ##molecule_type DNA
##residues 1-205 ##label KUN
##experimental_source strain 168
                                                                                                                                                                                                                                                                                                                                                                                                       AND PRO OGRAWATA, N.: Mosecy, I.; Albertini, A.M.;
Alloni, G.; Ascredo, V.; Bertich, M.G.; Besaffere, P.; Bans,
Alloni, G.; Ascredo, V.; Bertich, M.G.; Besaffere, P.; Bans,
Alloni, G.; Ascredo, V.; Bertich, M.G.; Besaffere, P.; Bans,
Alloni, M.; Burneri, S.; Bouris, M.G.; Besaffere,
Bruschi, C. V.; Caldwell, B.; Copuno, V.; Carter, M. M.;
Choi, S. K.; Codan, J.J.; Connecton, I.; Cummings, M.J.;
Choi, S. K.; Codan, J.J.; Connecton, J.; Crand, G.;
Elrich, S.D.; Emerari, E.; Foulger, D.; Fritz, C.; Puiter,
M.; Fuite, V.; Funa, S.; Gallæri, A.; Galacron, M.; Gins,
M.; Fuite, V.; Funa, S.; Gallæri, A.; Galacron, M.; Gins,
M.; Fuite, V.; Funa, S.; Gallæri, A.; Galacron, M.; Gins,
M.; Fuite, V.; Funa, S.; Gallæri, A.; Galacron, M.; Gins,
M.; Fuite, V.; Funa, S.; Gallæri, A.; Harvood,
Galæspi, G.; Guy, B.J.; Haga, K.; Halch, J.; Harvood,
G. R.; Henaut, A.; Hibert, H.; Holsappel, S.; Rusman,
M.; Honat, A.; Hibert, H.; Holsappel, S.; Rusman,
M.; Horst, D.; Macer-Blanchard, M.; Main, C.; Mobayash,
M.; Gayar, M.; Gharra, M.; Modega, B.; Main,
M.; Gayar, K.; Gybara, A.; Godega, B.; Bart, S. H.; Patto,
M.; Gayar, K.; Gybara, A.; Godega, B.; Bart, S. H.; Patto,
M.; Pohl, T.M.; Porteclle, D.; Porvollk, S.; Rechon, E.;
Roche, S.; Rose, M.; Sadler, T.; Sach, J.; Schowska, A.; Sacrox, S.; Serrox, P.; Shin, B.S.; Soldo,
Schowska, A.; Sacrox, S.; Serrox, P.; Shin, B.S.; Soldo,
Schowska, A.; Sacrox, S.; Serrox, P.; Shin, B.S.; Soldo,
M.; Tackan, K.; Takenchi, H.; Tanakoshi, A.; Tanaka, A.;
Wandont, R.; Main, R.; Main, R.; Main, K.; Takencox,
M.; Macharla, M.; Marmerox, M.; Macharla, M.; Mannerox, M.; Macharla, M.; Markan, M.; Tanaka, A.;
Wandont, R.; Main, A.; Tanakoshi, A.; Tanakoshi, A.;
Wandont, R.; Main, A.; Main, K.; Toshikasa, H.; Mamorox, M.;
Manneri, P.; Wapa, A.; Mannerox, M.; Tanakoshi, A.;
Wandont, R.; Main, A.; Markan, M.; Tanaka, A.;
Wandont, R.; Main, A.; Markan, M.; Tanaka, A.;
Wandont, R.; Wandoni, A.; Tosakoshi, A.; Tanakoshi, A.;
Wandont, R.; Wandoni, A.; Tosakoshi, A.; Tanakoshi, A.;
Wandont, R.; Wandoni, A.; Tana
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Michiele, T.; Wattiau, P.; Brasseur, R.; Ruysschaert, J.M.;
Infect. Immun. (1990) 58:2840-7849
Secretion of Top proteins by Tersiniae.
Inces MIDI: 90334044
B1440
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myosin alkali light chain 3, ventricular and slow skeletal
muscle - rat
muscle - rat
MCLab; MCIv; myosin Li catalyric light chain, cardiac
muscle; ventricular myosin light chain 1
sformal_name Rattus norvegicus scommon_name Norway rat
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#length 182 #molecular-weight 20828 #checksum 1492
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yop20 protein 'tersinia enterocolitica
formal_name 'tersinia enterocolitica
15-7eb-1994 *eequence_revision 10-Row-1995 *text_change
09-5ep-1997
$14240
ydhx
#length 205 #molecular-weight 22536 #checksum 3012
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| Siddiqui, M.A.O. |
| Siddiqui, M.A.O. |
| Periasmy, M.: Wadgsonkar, R.: Kumar, C.: Kartin, B.J.:
| Siddiqui, M.A.O. |
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Qy 1142 NPALPSD 1148
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**egene**

**genetic_code def

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||||||||
Qy 735 VTGATDT 741
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||||||||
Qy 264 AAPEPER 270
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred. No. 132e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
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##status
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##molecule_type mRNA
##cross-references EMBL:X14812; NID:g56669; PID:g56670
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Nucleic Acids Res. (1996) 24:4420-4449
Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
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*Kommil_name Mycopiasma pneumoniae
ANCC 23942

- Teb-1197 *sequence_revision 25-Apr-1997 *text_change
23-feb-1497 **Apr-1997 **Canney**
23-feb-1497 **
569588 stype complete hypothetical protein YDR533c - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             873913 stype complete
polypeptide deformylase def - Mycoplasma
29342) (SGC3)
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#modified_site blocked amino end (Pro) (in mature form)
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superfamily calmodulin; calmodulin repeat homology
blocked amino end; calcium binding; cardisc muscle;
duplication; EF hand; muscle contraction; skeletal muscle
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translation not shown
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Pred. No. 1.32e+01;
0; Mismatches 0; Indels 0;
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Pred. No. 1.32e+01:
0: Mismatches 0: Indels 0:
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District, T.S.

Subblasion submitted to be DMBL Data Library, August 1995

description The Enquince of S. cerevisiae commids 8166, 9787, 9717, and

secresion 65588

secresion 6
                                                   RESULT 35
ENTRY
TITLE
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**sene cDB:TFPA; AVED

**serine strences CDB:512364; OMIN:600415

**map_position 8q11.1-9 (4q11.3)

**classification **superfamily cellular retinaldehyde-binding protein homology FEATURE 53-447

**second collular retinaldehyde-binding protein homology 53-447
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Qy 99 LKELVAR 105
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**Fresidues**
1-261 **Label DIJ
CLASSITICATION ***
**superfeasily adenovirus early ELA protein alternative aplicing; DNA binding; early protein;
KEYMORDS transcription regulation; sinc finger
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#iength 237 #molecular-weight 25670 #checksum 2153
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Sauthors Dijkema, R.; Dekker, B.M.M.; van Ormondt, H.; de Waard, A.;

Sjournal Meat J.; Boyer, H.W.

Sjournal Gene (1980) 117.287-299

Stitle Gene organic adenovirus type 7: the Ela region of weakly

Genes references MUI: 811317792

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esmolecule_type mRNA
esresidues 1.278 sslabel ARI
sscross-references GB:D49488
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#label CRB
#langth 278 #molecular-weight 31749 #checksum 9071
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alpha-tocopherol transfer protein - human
stormal_name Homo sapiens scommon_name man
15-Juli-1955 sasquence_revision 01-Sep-1995 stext_change
10-Qctt_1997
00/177 ftype complete
alpha-tocopherol transfer protein - human
fformal_name Hamo ampiens fcommon_name man
21-Dec-1990 sequence_revision 06-Jun-1997 stext_change
10-Oct-1997
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18-Dec-1981 stext_change
18-Deb-1991 sequence_revision 18-Dec-1981 stext_change
15-Feb-1997
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early ElA 26K protein - human adenovirus 7
early ElA 24K protein
stormal_name Mastadenovirus h7 scommon_name human adenovirus
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#formal_mame Saccharomyces cerevisiae
22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change
21-Nov-1997
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230 REAGVPL 236
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SUMMARY O.84; Score 7; DB 1; Length 261; Best Local Similarity 100.0%; Pred. No. 132+01; Indels 0; Gaps Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps Query Match 0.6%; Score 7; DB 2; Length 262; Best Local Similarity 100.0%; Pred. No. 1.32e+01; 1-163,195-261 edomain response regulator homology #label RRR\
#binding_site phosphate (Asp) (covalent) #status
predicted
#length 262 #molecular-weight 29926 #checksum 8162 \$75610 ftype complete hypothetical protein - Symechocystia sp. (PCC 6803) formal_name Symechocystia sp. pcc 6803 Pcc 6803 25-Apr-1997 stext_change 05-Dec-1997 noko, T. Sato, S., Rotani, H., Tanaka, A., Asamisu, E., Bakamura, Y., Miyojiam, N., Hitosawa, M., Sugitra, M., Basamoto, H., Kisura, T., Hoseuchi, T., Hatsuno, A., Miraki, A., Hatsaki, M., Matuo, K., Okimura, S., Shimpo, S., Takeuchi, C., Rada, T., Matanaba, A., Yamada, N.; 0

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Deng, H.
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Ataxia with isolated withmin E deficiency is caused by mutations in the alpha-tocopherol transfer protein. 852466

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85937 stype complete
conserved hypothetical protein AF7298 - Archaeoglobus
fulyidus
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fformal_name Archaeoglobus ffulgidus
05-Dec-1997 stext_change
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protec-1997

Klebk H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Melson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gvinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlawsge, A.R.; Graham, D.E.; Kyrykdes, M.C.; Prisischmann, R.D.; Guckenbush, J.; Lee, N.R.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adama, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McHell, L.K.; Radger, J.H.; Glock, A.; B.; Good, R. G.; Graham, J.D.; Weldman, J.F.; McLach, F. J. Coverbeck, R.; Goodyn, J.D.; Spriggs, J.F.; McLach, P.; Kalman, B.P.; Sykes, S.M.; Sadow, F.W.; McLach, P.; Kalman, B.P.; Sykes, S.M.; Sadow, F.W.; McLach, P.; Kalman, B.P.; Sykes, S.M.; Sadow, F.W.; McLach, R.P.; Domman, C.; Pulli, C.; Garland, S.A.; McGood, R.; M.; McCarl, M.; M.; McCarl, C.J.; France, C.N.; Smith, H.O.; Mocse, Manna, T.M.; Olsen, G.J.; France, C.N.; Smith, H.O.; Mocse, Manna, T.M.; Olsen, G.J.; France, C.N.; Smith, H.O.; Mocse, M.; Manna, T.M.; Olsen, G.J.; France, C.N.; Smith, H.O.; Mocse, M.; Manna, T.M.; Charland, G.J.; Prisco, C.N.; Smith, H.O.; Mocse, M.; Manna, T.M.; Olsen, G.J.; France, C.N.; Smith, H.O.; Mocse, M.; Manna, T.M.; M.; Manna, T.M.; M

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Best Local Similarity 100.0%; Pred. No. 123e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
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**Itte The logice genome sequence of the hyperthermophilic, erross-reference MID:98049343

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365 PSFLLSS 371
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ERBO J. (1993) 12:4053-4062
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to antimicrobial peptides in Salmonella typhimurium.
53:936
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hypothetical protein - Baudomonas aeruginosa
formal_name Pseudomonas aeruginosa
0-Feb-1955 #sequence_revision 20-Feb-1995 #text_change
09-5ep-1997
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slength 321 #molecular-weight 36083 #checksum 3845
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Rankor Name No. 8: Kotani, N.: Hirosava, N.: Sugura, N.:
Rankoro, S.: Hygina, N.: Hirosava, N.: Sugura, N.:
Rankoro, S.: Hantra, T.: Hosouch, T.: Matanno, N.:
Richardi, N.: Rankar, N.: Handor, N.: Chunura, S.: Simpo,
Richardi, N.: Rankar, N.: Ranco, N.: Okumura, S.: Simpo,
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fittle The complete genome sequence of Escherichia coli K-12.
ferosa-references MRID:9745617
feaccession H64877
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BARtner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, M.T.;
Burland, V.; Riley, H.; Collado-Videe, J.; Glasner, J.D.;
Broke, C.K.; Maylev, G.F.; Gregor, J.; Davis, N.R.;
Rode, C.K.; Maylev, G.F.; Gregor, J.; Davis, N.R.;
Kirkpatrick, H.A.; Goeden, K.A.; Rose, D.J.; Mau, B.; Shao,
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efformal,name Symechocystia sp.
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peptide transport system permease protein SapB · Escherichia
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translation not shown .
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#formal_name Methanobacterium thermoautotrophicum 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997

ACCESSIONS REPERENCE Pauthors

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Flournal J. Exp. Med. (1989) 170.1837-1856
Fittle Comparison of exon 5 sequences from 35 class I genes of the
Fittle State of exon 5 sequences from 35 class I genes of the
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Molecular cloning of a novel mana highly expressed in

hasmochromatotic human liver and proliferating cells.
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#formal_mame Homo sapiens #common_name man
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EMBO J. (1985) 4:3203-3207 Duplicated gene pairs and alleles of class I genes in the Qa2 region, of the murine major histocompatibility complex: a
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JOSEO, Ograswara, N.; Mosser, I.; Albertini, A.n.;
Alloni, G.; Aserwedo, V.; Bertero, M.G.; Bessiere, L.; Brans,
Alloni, G.; Aserwedo, V.; Bertero, M.G.; Bessiere, L.; Brans,
A.; Brunn, M.; Brignell, S.C.; Bron, S.; Broutilet, S.;
Bruschi, C.V.; Caldwell, J.; Connerton, I.; Cummings, N.J.;
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Daniel, R.A.; Denicor, F.; Devine, K.M.; Dusterhoeft, A.;
Ehlich, S.D.; Emmerson, P.; Devine, K.M.; Desterhoeft, A.;
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Fahret, C.; Ferreri, E.; Foliger, D.; Frite, C.; Flyicka,
S.Y.; Classer, P.; Goffenu, A.; Galieson, M.; Grand, G.;
Cuiseppi, G.; Guy, B.J.; Hage, K.; Halesh, J.; Harwood,
Cuseppi, G.; Guy, B.J.; Hage, K.; Halesh, J.; Harwood,
C.R.; Henaut, A.; Hibert, N.; Blaspel, S.; Hosono, S.;
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KEYWORDS FEATURE 1-19 311-327 SUMMARY

RESULT 45 ENTRY TITLE

PC4211 Stype fragment hepatocellular carcinoma complicating haemochromatotis protein - human (fragment)

Oy 1116 GSLRTAQ 1122

97 GSLRTAQ 103

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7: DB 2; Length 334; Pred. No. 1.32e+01; O; Mismatches O; Indels O; Gaps

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GENETICS

22/1: 112/1: 204/1: 299/1

CLASSIFICATION superfamily class I histocompatibility antigen;

KETWORDS glycoprotein: transmembrane protein; transplantation antigen

KETWORDS glycoprotein: transmembrane protein; transplantation antigen

#domain signal sequence #status experimental #label SIG\
#domain transmembrane #status predicted #label TRS
#length 314 #mblecular-veight 37924 #checksum 270

REFERENCE

**molecule_type

*journal

J. Exp. Red. (1987) 165:1358-1370
Tissue-specific expression of cell-surface Qa-2 antigen from a transferted Q7(b) gene of C578L/10 mice.

A46545

WA46545, G.L.; Sherman, D.H.; Calvin, S.; Allen, H.; Plavell, R.A.

protein
'XXXX',26,'Y',28-29,'XXX',33,'X',35,'XX',38,'XXXX',43,
'XX',46,'L',40-49,'XXXX',54,'X',56-57 @elabel SOL

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AND Schook!, M.J.: Uhr. J.W.: Vitetta, E.S.

#Sounnal Nature (1982) 266,759-761
#Fille Primary structural studies of the Os-2 alloantigen:
**Extractions for the evolution of the NHC.
**ALERO NATURE
*accession A60760
*accession Lype Protein 20, xxxx, 24, x, 26, x, 28-30, xxxx, 35, xx, 38 **label **residues 20, xxxx, 24, x, 26, x, 28-30, xxxx, 35, xx, 38 **label

alloantigens. A60760

ACCESSIONS REFERENCE *authors *submission

Gentles, S.; Churcher, C.M. submitted to the EMBL Data Library, July 1995

ORGANISM DATE

SSB159 stype complete
hypothetical protein SPACLP7, 14c - fission yeast
(Schlisosaccharomyces pombe)
stormal_name Schlisosaccharomyces pombe
11-ofan-1996 sequence_revision 01-Mar-1996 stext_change
515166
558168

GENETICS

*gene
*start_codon
SUMMARY

MTH894
TTG
slength 327 *molecular-weight 35896 *checksum

*cross-references M01
*accession E69219
**status pi

preliminary; nucleic acid sequence not shown; translation not shown

. ascreriol. (1997) 179:7135-7155

Deplete genome sequence of Methanobacterium
thermosutotrophicum Delta H: functional analysis and
comparative genomics.

H MID:98037514

R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.;
J.; Aldredge, T.; Bashiradch, R.; Dakely, D.;
Gilbert, K.; Harrison, D.; Hoang, L.; Resgle, P.;
R.; Potchier, B.; Qiu, D.; Spedafors, R.; Vicette, R.;
V.; Herribowski, J.; Gibson, R.; Jiwani, N.; Caruso,
B.; D.; Safer, R.; Patvell, D.; Pashinakar, S.;
B.; D.; Safer, G.; Goyal, A.; Pietrobowski, S.;
J.; Montelais, G.J.; Mon, J.; Ricer, P.; Necling,
M.; Wantelais, G.J.; Mon, J.; Ricer, P.; Necling)

semolecule_type DNA earesidues 1-327 ##Label MTH ##Cross=references GB:AE000666 ##EXPERIMENTAL_BOURCE Strain Delta H

Query Match 0.69; Score 7; DB 2; Length 327; Best Local Similarity 100.00; Pred. No. 1.32+01; Matches 7; Conservative 0; Mismatches 0; Indels 0;

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103 EAGVPLG 109 |||||||| 231 EAGVPLG 237

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**molecule_type DAA
**residues 1-342 **label KUN
**residues 1-342 **label KUN
**caperimental_source strain 168
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S5795. Type complete
Protein VIU023c - yeast (Saccharomyces
hypothetical protein VIU023c - yeast (Saccharomyces
ALTERNATE_NAMES hypothetical protein 7,122
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**Southors**

J. Biol. Chem. (1990) 265:20061-20064

**Citle Molecular cloning of the fivet-Leu-Phe receptor from neutrophils.

**Cross-references MUID:1036034

**Cross-references MUID:1036034

**Cross-references G. 1859021

**Rolleular_type mRNA

**Fooleular_type mRNA

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No. 1.32e+01; Best Local Similarity 0; Mismatches 0; Indels 0; Gaps
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ockmann, M.P.; Munger, W.B.; Koglosky, C.; VandenBos, T.;
Price, V.; Lyman, S.; Gerard, N.P.; Gerard, C.; Cerretti,
D.P.
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smap_Dosition_10L
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Search completed: Pri Dec 18 19:04:21 1998
Job time : 172 secs.
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etithe Molecular characterisation of the interleukin-8 receptor.
ecross-references MUID:91378994
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establecular forman.
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FREENCE 556793
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Homolecule_type DNA
Hrzesidues 1-348 ##label RES
1-348 ##label RES
Process references EMBL:E25478; NID:g396520; PID:g396521
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fformal_name Acospirillum brasilense
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RA SAGA T., TUNG J. 7-5, SHEN F.-H., BOYSE E.A.;
PROC. NATL. ACAD. SCI. U.S.A. 83:6540-6944(1986).
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RA BASCHEE W.C.;

RI AND SCHEEN CO.;

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RECURSION THE PRISE PRIVATE MOTIVATION THEORY RECURSIVE PROCESS.

RECURSION THE PRISE PRIVATE SERVICEMENT OF THE CO.;

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MEDILINE; 87092355.

MASCHEW W.C.;
PROC. NATL. ACAD. SCI. U.S.A.
-1- FUNCTION: REQUIRED FOR T-C
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TISSUET-TCELL;
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REVISIONS:
SAGA I., TUNG J.-S., SHEN F.-W., BOYSE E.A.;
PACC. NATL. ACAD. SCI. U.S.A. 84:1991-1991(1987)
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DR PIN. A2562; A2552.

DR PIN. A2562; A2552.

DR PROSITE; PROGREDORIANED BY THE ACTIVATED CATALUTIC CHAIN.

DR POSITE; PROGRED STATE

DR PROSITE; PROGRED STATE

DR PROSITE; PROGRED; CARP_BINDING_1; PARTIAL.

DR PROSITE; PROGRED; CARP_BINDING_1; DARTIAL.

DR PROSITE; PROGRED; CARP_BINDING_1; ALTIVATION MULTICENE FAMILY.

DR PROSITE; PROGRED; CARP_BINDING_1; ALTIVATION MULTICENE FAMILY.

DR PROSITE; PROGRED; CARP_BINDING_1; ALTIVATION MULTICENE FAMILY.

PRI NOMA, TER 1 DIMERIZATION AND PHOSPHORYLATION.

PT NOMA, TER 2 1 DIMERIZATION GPT SIMILARITY).

PT NOMA, TER 3 2 > 15 CARP.

PT NOMA, TER 15 15 CARP.

PT NOMA, TER 15 15 15 CARP.

PT NOMA, TERM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dec
                                                                                                                Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 8; Conservative
52 EEEDTDPR 59
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461 EEEDTDPR 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: FOUR TYPES OF F
I-ALPHA, I-BETA, II-ALPHA, AND II-E
AMONG TISSUES AND IS IN SOME CASES
INDUCTRIE
                                                                               1998
                                                                                                                     Score 8; DB 1; Length 155;
Pred. No. 4.71e-02;
O; Mismatches O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGULATORY CHAINS ARE POUND:
-BETA. THEIR EXPRESSION VARIES
S CONSTITUTIVE AND IN OTHERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-951-733-20.rsp
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ACT_SITE
ACT_SITE
CARBORYD
CARBO

PROTEIN-TYROSINE PROSPHATASE.
BY SIMILARITY.
BY SIMILARITY.
ROTENYIAL.
POTENYIAL.

COCCOOCUERA RAMAN COCCOCUERA RAMAN COCCOOCUERA RAMAN COCCOCUERA RAMAN COCCUERA RAMAN COCCOCUERA RAMAN COCCUERA RAMAN COCU

SECURNE FROM N.A.

KEDLINE: 87080758A.

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FERS LETT. 709:119-222(1986).

1 FUNCTION: TIPE II REGULATORY CHAIRS, INCLIDING THE MAP2 KINSE.

1 SUBUNIT: THE INACTIVE FORM OF THE ENTRYME IS COMPOSED OF TWO

1 SUBUNIT: THE INACTIVE FORM OF THE ENTRYME IS COMPOSED OF TWO

1 SUBUNIT: THE INACTIVE CATALITIC CHAIRS. ACTIVATION BY CAMP

PRODUCES TWO ACTIVE CATALITIC MONOMERS AND A REGULATORY DIMER

THAT BILDS FOUR CAMP MOLECULES.

DESCRIPTION OF STANDARD; PRT; 155 AA. .

(DESCRIPTION OF STANDARD; PRT; 155 AA. .

(C) 105207.

(T) 1.4MG.1987 (REL. 05, CREATED)

(T) 1.7EB.1986 (REL. 33, LAST SECUENCE UPDATE)

(T) 1.7EB.1996 (REL. 33, LAST ANNOYATION UPDATE)

(T) 1.7EB.1997 (REL. 05, LAST ANNOYATION UPDATE)

(T) 1.7EB.1997 (R

CHAIN

RESULD 4

DE COLVANA-1988 (REL. 10. CREATED)
DT 01-MAR-1988 (REL. 10. CREATED)
DT 01-MAR-1988 (REL. 10. LAST RECURENCE UPDATE)
DT 15-UT-1998 (REL. 10. LAST RECURENCE UPDATE)
DT 15-UT-1998 (REL. 10. LAST RECURENCE UPDATE)
DR UNALIL-DHA GLYCOSTLASE (RC 3.2.2.) (UDG).
CN 53.
CN VIRICELLA-COSTEN VIRUS (STRAIN DUMAS) (VEV).
CC VIRICELS 19-NAN AMPLIADED VIRUSES; HERDESVIRIDAE; ALP
RN 111
RP SEQUENCE PRON N.A.
RX MEDILIRE; 68-306657.
RA DAVISON A.J. SCOTT J.E.;
RL J. CRN. VIROL. 67:1159-1816(1986).
CC 1- RESULT OF MEDICINE MORALINATION OF DUME RESIDUES
CC 1- SUCHEMBAR OR DE TO DEMINISTRON OF CUTOSINE.
DR PROSITE; P800110; U_DNA_GLYCOSYLASE; 1.

ALPHAHERPESVIRINAE

(1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM THE DIA WHICH CAN ARISE
1- FUNCTION: SECUES MACKET RESIDUES FROM THE DIA WHICH CAN ARISE
1- FUNCTION: EXCUSES MACKET RESIDUES FROM THE DIA WHICH CAN ARISE
AS A RESULT OF MISSINGORPORATION OF DUMPH RESIDUES BY DIA
DOLMERASE OR DUE TO DEMINIATION OF CYTOSIZE.
1- SINILARIY: BELONGS TO THE URACIL-DRA GLYCOSTIASE FAMILY.
EMBL. X04370; 660048 - .
DIR: G37215, DGESS.
PROSITE: PSO0130: U_DNA_GLYCOSTIASE; 1.

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8 LAPGFALLD 16 |||||||| 119 LAPGFALLD 127

Query Match 0.8%; Best Local Similarity 100.0%; Matches 9; Conservative

Score 9; DB 1; Length 1152; Pred. No. 2.00e-04; 0; Mismatches 0; Indels

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Gaps

130421

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J.-S.,

CANTOR

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DNA REPAIR, HYDROLASE, GLYCOSIDASE,
ACT.SITE 146 148 GENERAL BASE (BY SIMILARITY)
SEQUENCE 305 AA; 34376 MM; ODD3B64F CRC32;
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Page 25

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Page 26

CAN2_BOVIN STANDARD; PRT; 400 AA.

90313; 1986 (REL. 01, CREATED)
21-701-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEE-1996 (REL. 31, LAST ANODATION UPDATE)
01-FEE-1996 (REL. 31, LAST ANODATION UPDATE)
CAN2-DEPENDENT PROTEIN KINASE TIPE 11-ALPHA REGULATORY CHAIN.

PERAPA. BOS TARROS (BOVINZ). BUILANTOTA: METAGOA: CHORDATA; VERTEBRATA: TETRAPODA: HAMMALIA; ETTHERIA; ARTIODACTILA.

TISSUE-HEART MUSCLE: MEDLINE; 82222175. TAKIO K., SMITH S.B., E PROC. NATL. ACAD. SCI. PROC. NATL.

KREBS E.G., WALSH K.A., TITANI K.; . U.S.A. 79:2544-2548(1982).

STRUCTURE MODELLING.

Query Match 0.7%; Score 8; DB 1; Length 305; Best Local Similarity 100.0%; Pred No. 4.71e-02; Matches 8; Conservative 0; Mismatches 0; Indels 0; 231 RVLQRLCE 238 [|||||| 105 RVLQRLCE 112 Caps

TMOS_MSVTS STANDARD; PRT; 342 AA.
P10421;
01-MR-1999 (REL. 10, CREATED)
01-MR-1999 (REL. 10, LAST EQUINCE UPDATE)
01-MR-1999 (REL. 10, LAST SCOURNCE UPDATE)
101-MR-1999 (REL. 12, LAST ANNOTATION UPDATE)
101-MR-1999 (REL. 12, LAST ANNOTATION UPDATE)
100-SERINE/THREONINE-PROTEIN KINASE TRANSPORMING PROTEIN (EC 2.7.1.-). PELOPROLIFERATIVE SARCOMA VIRUS (CLOME TS159). (RIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE: COVIRIMAE.

WEDELIE, 8715/645.
WEDER I.T., STEIT T.A., BUBIS J., TAVIDR S.S.;
WEDER I.T., STEIT T.A., BUBIS J., TAVIDR S.S.;
BICCHEMISTRY 26:143-251(1987).

1- SERBHYI THE IMACTURE PORM OF THE ENEYME IS COMPOSED OF TWO
REGILATORY CHAINS AND TWO CATALTTIC CONDUCES AND A REGULATORY DIMER
PRAY BINDS PORM CAMP POLECULES,
THAT BINDS POLECULE

SECURNIC FROM M. A.

*** SECURNIC G., STACEY A., OSTERTAG W.;

*** J. VIROL. S.: 889-997(1987).

*** J. VIROL. S.: 189-997(1987).

*** ON STATE ON SERVED CATALYTIC DOMAINS OF SER/THR-COMPONIC SERVED CATALYTIC DOMAINS OF SER/THR-COMPONIC SERVED. MI444; G33221;

*** PROSITE: PROSULO: PROTEIN LINASE_ATP: 1.

*** PROSITE: PROSULO: PROTEIN LINASE_ATP: 1.

*** PROSITE: PROSULO: PROTEIN LINASE_ST: 1.

*** PROSITE: PROSITE: PROTEIN LINASE_ST: 1.

*** PROSITE: PROSITE: PROSIT

63 69 90 198 342 AA; 338 77 90 198 B 37970 MH; PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
MM; 1056243C CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 342; Pred. No. 4.71e-02; 0; Nismatches 0; Indels Indels 0 Caps

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MANNET TISSUES AND IS IN SOME CARES CONSTITUTIVE AND IN VARIOUS
TINDCITIES
THE A SECOND PROSPRORTATION SITE BAS NOT BEEN LOCATED.
THE A MODEL TO THE A SECOND PROSPRORTATION SITE BAS NOT BEEN LOCATED.
THE A MODEL TO THE A SECOND PROSPRORTATION SITE BAS NOT BEEN LOCATED.
THE ADDITION OF THE ADDITION OF

291 LRPSLTGA 298 |||||||| 372 LRPSLTGA 379

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343 C 343 C CAMP. CAMP. : 197A0D99 CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Leng Pred. No. 4.71e-02; 0; Mismatches 0; Length 400; Indels

LAPA_EUNAM STANDARD; PRT; 403 AA.

P1161: 016821;
01-2AN:1990 (REL. 13, CREATED)
01-2AN:1990 (REL. 13, CREATED)
01-2AN:1990 (REL. 13, LAST ANNOCATION UDDATE)
01-3AN:1990 (REL. 36, LAST ANNOCATION UDDATE)
CAMP-DEPENDER;
02AN:0-DEPENDER;
02AN:0-DEPNDER;
02AN:0-DEP

TISSUE-TESTIS: 1. A. TISSUE-TESTIS: 1. A. TISSUE-TESTIS: 1. SCOTT J.D., HANSSON V., PEBS LETT. 246:57-64(1989). JAHNSEN

SECURNCE OF 1-65 FROM N.A.

WESTLINES JIJSORIE R., SIAMED J., MYKLEBUST F., RANSSON V.,

A. ANDREM T., TASKEN K.,

BIOCHIM. BIOPHYS. ACTA 135:09-108(1997).

C. I. FUCCTION: TIPE IL REGULATORY CHEINS MEDIATE MEMBRANE ASSOCIATION

EN BIDDING TO ANCHORING PROTEINS, INCLIDING THE MAP KINASE.

C. I. SUBURIT. THE INACTURE FORM OF THE EXITE IS COMPOSED OF TWO

C. REGULATORY CHAINS AND TWO CATALITIC CHAIRS. ACTIVATION BY GAMP

PRODUCES TWO ACTIVE CATALITIC MONOMERS AND A REGULATORY DIMER

C. I. TISSUE SPECIFICATI FOUR THE SERVER AND A REGULATORY FORDS.

C. I. SUBURIT. SPECIFICATI FOUR THE SERVER AND A REGULATORY FORDS.

ANOMET INSURED THAT IN THE ANGEN CASES CONSTITUTIVE AND IN OTHERS.

ANDRET TISSUES AND IS IN SOME CASES VARIANTES CHAIN.

INDOCEME.
EMBL. X14966; 239448; EMBL. X199455; 235455; EMBL. X99455; 235455; EMB. S010855 OKUCHA.
HSSP. P00515; AAPK.

BINDING 343 BINDING 343 SEQUENCE 400 AA;

0 Caps 0

106 EEEDTDPR 113 |||||||| 461 EEEDTDPR 468

VERTEBRATA; TETRAPODA; MAMMALIA;

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ENZYME)

MAN: 176910: -.
PROSITE: PROOBES;
PROSITE: PSO0889;
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PROSITE: 10
PROSITE: 10
PROSITE: 10
PROSITE: 207
; CNMP_BINDING_1; 2. ; CNMP_BINDING_2; 2. ; CNMP_BINDING_3; 2. OSPHORYLATION; DUPLICATION;

HULTIGENE FAMILY:

346 45387 MN; ACEPTATION (BROBABLE),
PROSPHORTLATION (BY SIMILARITY).
CAMP.
CAMP

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative Score 8; DB 1; Length 403; Pred. No. 4.71e-02; 0; Mismatches 0; Indels .

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109 EEEDTDPR 116 |||||||| 461 EEEDTDPR 468

HEST, LEAST STANDARD: PRT: 654 AA.

P11398
01-007-1999 (REL. 12, CREATED)
01-007-1999 (REL. 12, LAST SEQUENCE OFDATE)
01-007-1999 (REL. 14, LAST SEQUENCE OFDATE)
01-007-1999 (REL. 14, LAST SEQUENCE OFDATE)
MITOCHOMBRIAL HEAT SHOCK PROFERM SCI PRECURSOR (ENDOWUCLEASE OF DISCONDENSIS)
SECTION ENSI OR MITOGRAFIE (BARREY OF TEAST),
FUNANTURAL FUNCTION ADMINISTRATION OF TEAST (FINANCIAL PROMETTES.)

SCZI

SENOTENCE FROM N.A.
SENOTENCE FROM N.A.
SENOTENCE FROM N.A.
HOLMES 5.,
KEDLINE, 89384560.
CRAJE E.A., RAMARE J., SHILLING J., WERNER-WASHBURNE M., HOLMES 5.,
KOSIC-SHITHERS J. NICOLET C.M.
MOLI. CELL. BIOL. 9.3000-3008(1989).

SEQUENCE FROM N.A., AND SEQUENCE OF 24-41. STRAIN-IAM 4274; MEDLINE: 90368701.

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MORISHIMA N., NAKAGAWA K., YAMAMOTO E., SHIBATA T.;
J. BIOL. CHEM. 265:15189-15197(1990).
SEQUENCE FROM N.A.
STRAIN=S288C;
WEDLINE; 95397595.
WEDLINE; 95397595.
GRAT J.-C., GALIBERT
FEAST 11:775-781(1995).
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SENGURNE OF 24-38.

KEDLINE, 91092254.

SCHEMER P. E., KRIEG U.C., HWANG S.T., VESTWEBER D., SCHATZ G.;
ERBO J. 9:4315-4422(1990).

SHORTON: SSCI IS AN ESSENTIAL MITOCHONDRIAL PROTEIN, IT

HAY PLAY A ROLE IN FACILITATING THE ASSEMBLY OF SOME PROTEIN

THAT PLAY A ROLE IN SCHLITATING THE ASSEMBLY OF SOME PROTEIN

THAT PLAY A ROLE IN SCHLITATING THE ASSEMBLY OF SOME PROTEIN

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ID DPOK_ARATI
AC P30322;
AC P30322;
DT 01.APR.1193

01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
PRODALE DNA POLYMENSE (EC 2.7.7.7) (FRACHENT).
AGRICCOS SITOROUIS.
MITOCHONDRION.
PLASHID PEM.
PLASHID PEM.
PLASHID PEM.

STANDARD;

PRT;

797 AA.

RE SECURICE PROM N.A.

RE SECURICE PROM N.A.

RE SECURICE PROM N.A.

RE MEDITION 1914560 / AG4;

RE MEDITION 1914560 / AG4;

RE MEDITION 1914560 / AG4;

RE MEDITION N. BOYER J.C., HORGEN P.A.;

RE CORR. GENET. 19145-502(1991).

CC IN PYROPHOSPHATE + DNA(N).

CC IN PROPHOSPHATE + DNA(N).

RE ENGLY MAG107; GENERAL AND PLANTS HITOCHONDRIAL PLASHIDS.

CR ENGLY MAG107; GENERAL PROPHOSPHATE PROPH

SPACE
INSTRUCEMENTAR LOCATION. MITOCHONDRIAL MATRIX. DETECTED ALSO IN THE
NUCLEUS AFTER HEAT-SHOCK.
THE HEAT SHOCK DECK PROTEIN 70 FAMILY. STRONGEST
SINLLARITY WITH OTHER MITOCHONDRIAL HSP70 AND WITH BACTERIAL DHAK.
EMBL. MATZ39, G171089;
EMBL. MATZ39, G171083;
EMBL. L18644, G119703;
EMBL. L18646,
SGD: LOUGHSE: SGC1.

PROSITE: PRO1379: HSP70_1: 1.

PROSITE: PRO1379: HSP70_2: 1.

PROSITE: PRO1379: HSP70_2: 1.

PROSITE: PRO1379: HSP70_2: 1.

PROSITE: PRO1379: HSP70_2: 1.

PROSITE: PRO1379: HSP70_SCR.

ALTOCHOMBRICH: MITCHOMBRICH: MITCH 24 634 643 650 654 AA; 23 24 654 4 646 646 650 70627 MH; HEAT SHOCK PROTEIN SSC1.
HEAT SHOCK PROTEIN SSC1.
ASS+RICH.
ASS+RICH.
N > NN (IN REF. 2).
N -> D (IN REF. 2).
G -> D (IN REF. 2).
M4; 0EB32F62 CRC32;

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative 595 LKELVARV 602 |||||||| 99 LKELVARV 106 Score 8; DB 1; Length 654; Pred. No. 4.71e-02; 0; Mismatches 0; Indels ö Gaps 0

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RE SÉQUENCE OF 491-968 FROM N.A.

RE SEMENTIFIE MAY-1995) TO BREA-GENERAIR/DEBJ DATA BANES.

RE SUBMITTIES MAY-1995) TO BES-GENERAIR/DEBJ DATA BANES.

RE SUBMITTIES MAY-1995) TO BES-GENERAIR MOSCIE, BEART, KIDNET,

CO -- THE SEMENT CHITT: BHAIN, SEGLETAL MOSCIE, BEART, KIDNET,

CO -- LINGUIS BESETICITT: BHAIN, SEGLETAL MOSCIE, BEART, KIDNET,

CO -- LINGUIS BESETICITT: BHAIN, SEGLETAL MOSCIE, BEART, KIDNET,

CO -- LINGUIS BESETICITY: BHAIN, SEGLETAL MOSCIE, CANTON CHINALARIT,

SYNDROME DEFECTION CHINALES BESTANT RICKETS, ANIMOACIDURIA,

CO -- LINGUIS BESINGE TO THE INCSITUL-1,4,5-TRISPHOSPHATE

SPROSHATASS TO THE MINISTITUL-1,4,5-TRISPHOSPHATE

SPROSHATASS TO THE MINISTITUL-1

Score 8; DB 1; Length 968; Pred. No. 4.71e-02; 0; Mismatches 0; Indels Ö Gaps

0

EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; PRIMATES. VERTEBRATA; TETRAPODA; MAMMALIA; US-08-951-733-20.rsp

SEOCINCE FROM N.A. TISSUP-KIDENT; HEDLINE; 9331440. ALTREE O., OLIVOS I.M., OKABE I., BAILEY L.C., NELSON D.L., LEWIS R.A., MCINES R.R., NUSSBACH R.L.; MATTREE 358:139-147(1991).

HTDROLASE.

CONFLICT 660 660 G -> E (IN REF. 2).

CONFLICT 968 AA: 111485 MW; 53CE3BE2 CRC32;

ő B 30 LPAPGARR 37 |||||||| 238 LPAPGARR 245

Query Match 0.7%; Best Local Similarity 100.0%; Matches 8; Conservative

EX SOLUTION OF PROPERTY OF SOLUTION OF SOL SRUT 10

PRINI YAST STANDARD; PRT; 1480 AA.

PRISCIPLE STANDARD; PRT; 1480 AA.

PRISCIPLE STANDARD; PRT; 1480 AA.

PRINI PROTEINS (REL. 27, CREATED)

PANI PROTEINS (REL. 35, LAST SEQUENCE UPDATE)

PANI PROTEINS (REL. 35, LAST ANNOTATION UPDATE)

PANI PROTEINS (REL. 37, LAST ANNOTATION UPDATE)

PANI PROTEINS CREEVISTAE (BARET'S YEAST).

SACCHARONICS CREEVISTAE (BARET'S YEAST).

SACCHARONICS CREEVISTAE (BARET'S YEAST). SEQUENCE FROM N.A., AND SEQUENCE OF 320-344; 352-375 AND 899-906. MEDLINE; 92405166.

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Mon Dec

SACHS A.B., DEARDORFF J.A.; CELL 70:961-973(1992).

SENDENCE PROM N.A.
SENDENCE PROM N.A.
SENDENCE PROM N.A.
SENDENCE PROMITER A.T., BORMAN S., BROWN D.,
CHIDCHER C.M., CONNOR R., CONSET T., DEAR S., DEFLIE K., PRASER R.
GENTLES S., LIZE G., MOTILE S., MOTILE T., ODELL C., PRASEO D.,
NAMEDIAM M.A. BELES L., ROWLET N., SKILTON J., SRITH Y.,
NAMEDIAM M.A. BELES L., ROWLET N., SKILTON J., SRITH Y.,
SUMMITTED (DE. 7.1944) TO EMBL/GENBANK/DDBJ DATA BANKS.

* ?

J., TEODORU C., VALENCIA A., SENSEN C., WIEMANN S., MERMANN J., SANDER C., ANSORGE W.;

OF PAB-DEPENDENT

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APPROXIMATE REPEATS.

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RESULT DT 01 OC QC GN CL11

CCELL_HUMAN STANDARD: PRT: 968 AA.
Q01968; Q15684; Z15684; Z6, CREATED)
Q1-701-1993 (REL. 26, LAST SEQUENCE UPDATE)
Q1-701-1994 (REL. 26, LAST SEQUENCE UPDATE)
L5-701-1998 (REL. 26, LAST ANDORATE PROTEIN.
CCEL. STANDARD: STANDARD PROTEIN.
COMB. SAPIENS (HUMAN).

B

670 SSYARTSI 677 |||||||| 969 SSYARTSI 976

Query Match 0.79; Score 8, DB 1; Length 797; Best Local Similarity 100.0%; Pred. No. 4.71e-07; Matches 8; Conservative 0; Mismatches 0; Indels

Indels

0 Caps

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NON_TER 1 1 SEQUENCE 797 AA; 91922 MW; 2D4D4AB9 CRC32;

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(CGF-SIDDING PROTEIN 2) (FRAGMENT). 1GFB-2. 1GB SCODA, (FIG). EUGANOTA, MITANOA, CHORDATA; VERTEBRATA; EUTHERIA, ARTIODACTILA.

TETRAPODA;

MANMALIA

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ID AC P2
DT 011
DT 011
DT 011
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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P24853:
01-MAR-1992 (REL. 21. CHEATED)
01-MAR-1992 (REL. 21. LAST SEQUENCE UPDATE)
01-FER-1995 (REL. 21. LAST SEQUENCE UPDATE)
101-FER-1995 (REL. 31. LAST SEQUENCE UPDATE)
118GULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 (ICPBP-2) (IBP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AAPEPER 39
|||||||
264 AAPEPER 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET 0 0 O NOW TER 51 51 SEQUENCE 51 AA; 5085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 09:28:29 1998
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||||||||
439 AAVTPAAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 1480 AA;
                                                                                                                                                                                                                     SPRAINS-SHEC, A.8971
STRAINS-SHEC, A.8972
STRAINS-SHEC, A.8972
STRAINS-SHEC, A.8973
DOBISTON H. ADDRESS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
DOBISTON H. ADDRESS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
DOBISTON H., ADDRESS S., BRINKMAN R., CESSEL C.,
KOCARA T., HILLER L., JUER H., JOHNSTON L., LANGSTON Y., MODSER L.,
LATREILLE P., LOUIS E.J., MORRI C., MARDIS E., METERES S., MODSER L.,
MANN H., RIKKH L., RILES L., ST PETER H., TRYASKIS E., VAUCHAN K.,
VIGNATI D., WILCON L., WOHLDMAN P., WATERSTON R., WILGON R.,
VALUEN H.)
                                SEROCIENCE FROM H.A. (YANGGO).
STRAIN-S28G J. AB972;
BURSET H., KEWG T., STORMS R.K., YO D., ZHONG W., FORTIN N.,
BARTON A.B. KARACK D.B., CLARK M.W.; DDBJ DATA BANKS.
SUBHITTED (FEB-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                         IENCE 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160267
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Pred. No. 5.98e+00;
0; Mismatches 0; Indel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8: DB 1; Length 1480;
Pred. No. 4.71e-02;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4EC3AC9B CRC32;
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RESULA 14

DESCRIPTION STANDARD; PRT; 139 AA.

AC PO4437; AND 1997 (REL. 05, CREATED)

DT 11-AGC-1997 (REL. 05, CAST ESDORECE UPDANTE)

DT 11-AGC-1997 (REL. 05, CAST ESDORECE UPDANTE)

DT 7-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (CTL-L17).

CS HOND GAPIENS (TUMAN)

CS EUTARCOTA; METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA

CS EUTARCOTA; PATAMATES.

RM 1502BMC FROM H.

RM 1502BMC FROM H.

RM 2502BMC FROM J.

RM 17-RELL; PATAMATES.

RM 1502BMC FROM J.

RM 17-RELL; PATAMATES.

RM 18-RELL; PATAMA
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RECOURSE, 92109718.

RA MEDLINE, 92109718.

RA RASTIEL, 93109718.

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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1126 SRKLPGT 1132
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105471989 (REL. 10, CERATED)
01-MAR-1989 (REL. 17, LAST ESCORECE UPDATE)
01-FED-1991 (REL. 13) LAST ANSOCRATION UPDATE)
101-FED-1996 (REL. 33) LAST ANSOCRATION UPDATE)
MOSIN LICHET CHAIN 1, SION-TWITCH MUSCLE BYVENTRICULAR ISOFORM
MOSINGEOLUS (MOUSE)
MIL OR MACULE
MIL OR MACU
                                                                                                                                                                                                                                                                                                                                                                                                                               TCRA.
HONO SAPIENS (HUMAN).
EUNANCOTA; METADODA; CHORDATA; VERTEBRATA; TETRADODA; MANNALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C3H; TISSUE-SPLZEN;
MEDLINE: 89057447.
COMEN A., BARTON P.J.R., ROBERT B.,
BUCKINGHAM M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 RPPPAAP 21
|||||||
85 RPPPAAP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 1; Length 111;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 1; Length 23;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARNER I., ALONSO S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UB-08-951-733-20.
                                                                                                                                                                                                                                                                                                                              I-LYMPHOCYTE
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HPCR_ECOLI
AC Q07095;
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CC SUTANDE CA. PROSENTE VIA. 6.7-DIRTERICATION AND 1-3.4-DIRTERSENT.
CC SUTANDE CA. (114.38) - PERMIDIDIRECTOR OF 5. HARD CA. (1.27) - RESTRICT.
CC ALIANO 2.4 (114.38) - PERMIDIDIRECTOR OF 5. HARD CA. (1.27) - RESTRICT.
CC -1-CADALTE VIENDAMO. 6.7-DIRTERIUS -1-LO-REBITTI-LOMBERS.
CC -1-CADALTE A. (1.13-REBITTI-LOMBERS. C. 1.13-REBITTI-LOMBERS. C. 1.13-REBITTI-LOMBERS. C. 1.13-REBITTI-LOMBERS.
CC -1-CADALTE S. FANAL STEP OF RESOFTATIS SYMPHESIS.
CC -1-SHILMITI OLICOMERS TRAT CONSIST OF 3. HARD SUBMITIS AND 60 BETA.
CC -1-SHILMITI OLICOMERS TRAT CONSIST OF 3. HARD SUBMITIS AND 60 BETA.
CC -1-SHILMITI SELONGS TO THE DUAL SYMPHASE PAMILY.
DR CHAIL SEDICITE SELONGS TO THE DUAL SYMPHASE PAMILY.
DR CHAIL SEDICITE SELONGS TO THE DUAL SYMPHASE FAMILY.
SERVINE BECOMES TO THE WORLD STANDARD CONTROL OF STANDARD STANDARD TRANSPERSARE, TANDARD CONTROL OF STANDARD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTECTION BEGLIATOR FROM PARTIES FROM STATEMENT OF TRANSCRIPTION SECURISTICS FROM PROTECTION REPRESSOR FOR THE MORNER FAMILY OF TRANSCRIPTIONAL CARBOLIC FROM PROTECTION REPRESSOR FOR THE MARR FAMILY OF TRANSCRIPTIONAL CARBOLIC FROM PROTECTION PROTECTIO
                                                                   Ouery Match 0.0%; Score 7; DB 1; Length 155; Best Local Similarity 100.0%; Pred. No. 5, 98e+00; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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No. 5. 998+09; Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5, 98e+00;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RR__SPIRO STANDARD: PRT; 155 AA.
PAJ342;
01-NOV-1995 (REL. J3. CREATED)
01-NOV-1995 (REL. J3. LAST SEQUENCE UPDATE)
01-FEE-1996 (REL. J3. LAST SEQUENCE UPDATE)
01-FEE-1996 (REL. J3. LAST ANNOVATION UPDATE)
CHICROPLAST 30S RIBOSOMAL PROTEIN S7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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SEQUENCE 139 AA; 15441 MW; 8EAE2341 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LLGASVL 10
|||||||
|697 LLGASVL 703
                                                                                                                                                                                                                                                                                                                            SEOURNE FROM N.A.

LEM K.A., MANIART J.R.;
J. BRYCOL. 29:500-505(1931).

-1- SIMILARTI, BELONGS TO THE S7P PAMILY OF RIBOSOMAL PROTEINS.

BEBLI, LO7932; C470152;
-1- SEMILARTIE, PS00512; RIBOSOMAL, S7; 1.

RIBOSOMAL PROTEIN: CHICAROPLAST;

SCOURNE 153 AX; 17769 MR; 6958C1AB CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 09:28:29 1998
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|||||||
124 ALLDGAR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINS-C;
STRAINS-C;
RODER D.I., FANCETT T., COOPER R.A.;
RODER D.E., FANCETT T., COOPER R.A.;
ROL. GEN. GENET. 237:241-250(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (REL. 11. CREATED)
01-FEB-1995 (REL. 131. LAST SEQUENCE UPDATE)
01-FOW-1997 (REL. 355. LAST ANNOTATION UPDATE)
ROMOPROTOCATECHNATE DEGRADATIVE OPERON REPRESOR.
HUCR OR HPAR.
BECHERICHIA COLI.
BECHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UKARYOTA: PLANTA; PHYCOPHYTA; CHLOROPHYTA (GREEN ALGAE);
ONJUGATOPHYCEAE; ZYGNEMATALES; ZYGNEMATINEAE; ZYGNEMATACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIROGYRA MAXIMA
HLOROPLAST
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 7; Conservative
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P27474;

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P71655;
01-80V-1997 (REL. 35, CREATED)
01-80V-1997 (REL. 35, LAST EXCURINCE UPDATE)
01-80V-1997 (REL. 35, LAST EXCURINCE UPDATE)
01-80V-1997 (REL. 35, LAST EXCURINCE OPDATE)
01-80V-1997 (REL. 35, LAST ANNOVATION UPDATE)
01-80V-1997 (REL. 35, LAST ANNOVATION UPDATE
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STALTS-SITAN;
STALTS-SITAN;
STALTS-SITAN;
SUBMITTED (AR-1396) TO EMBL/GENBANK/DDBJ DATA BANKS.
1- STALTAETT; BELGANG TO THE AHDC/TSA FAMILY.
EMBL; 270692; EMISSOS) - OF STALTAETT;
BELGANG TO THE AHDC/TSA FAMILY.
EMBL; 270692; EMISSOS) - OF STALTAETT AND STALTAET
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05444.
05444.
05444.
05444.
01-80V-1997 (REL. 35, CREATED)
01-80V-1997 (REL. 35, LAST SECURECE UPDATE)
01-80V-1997 (REL. 35, LAST ARROTATION UPDATE)
CROSSOVER JUNCTION ENCONDATELEMORETURES RUYC (RC 3.1.22.4) (SOLLIDAY UNCTION RESOLVASE RUYC).
RUYC.
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113 RGAKNVL 119
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010520;
01-007-1996 (REL. 34, CREATED)
01-007-1996 (REL. 34, LAST EMODRATE UPDATE)
01-007-1996 (REL. 34, LAST EMODRATE UPDATE)
01-007-1996 (REL. 34, LAST EMODRATE)
RPOPHERICAL 16.8 M PROFILE (Y427.19C.
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PROXARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
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PROMANYOPA: GRACILICUTES: SCOTOBACTERIA: AEROBIC RODS AND COCCI;
PSEUDOMONADACEAE.
         (REL. 23, CREATED)
(REL. 23, LAST SEQUENCE UPDATE)
(REL. 26, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                            STANDARD;
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 1; Length 153;
Pred. No. 5.98e+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  PRT;
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YOPQ PROTEIN PRECURSOR. YOPQ OR YOP2O. YERSINIA ENTEROCOLITICA. PROLANTO PYV. PROLANTOPA: CRACLICUTES; SCOTOBACTERIA; PACULTATIVELY ANAEROBIC RODS; PRIEROBACTERIACEAE.

SEQUENCE PROM N.

STALEWISS SO / SEROTYPE 0:9;

HEDLIEE, 9034044

HIGHELS T. MATTIEAU P., BRASSEUR R., ROTSSCHAERT J.M., COI
INFECT. INCOM. SE. 2840-2849(1990).

INFECT. INCOM. SE. 2840-2849(1990).

INFECT. INCOM. SECRETED (PROBABLE).

PERL X527321, 448040.

PIR. 181440; 814340.

SIGNAL PATEMALA.

1 1 2 1 1840.

POTENTIAL.

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POTENTIAL.

CORNELIS

SIGNAL 1 24 POTENTIAL. CHAIN 25 182 TOPO PROTEIN. SEQUENCE 182 AA; 20828 MW; 2A32F684 CRC32;

Opery Match 0.6%; Score 7; DB 1; Length 182; Best Local Similarity 100.0%; Pred. No. 5.98e+09. Matches 0; Indels Matches 0; Indels <u>.</u>

62 GSILSTL 68 ||||||| 856 GSILSTL 862 Caps

0

8

29 AAPEPER 35 | | | | | | | | | 264 AAPEPER 270

HA19_MOUSE STANDARD; PRT: 200 AA.

P14431;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-UUL-1990 (REL. 15, LAST SATORDATED UPDATE)
15-UUL-1990 (REL. 15, LAST ANNOTATION UPDATE)
15-UUL-1990 (REL. 15, LAST ANNOTATION UPDATE)
15-UUL-1990 (REL. 15, LAST ANNOTATION UPDATE)
15-AGGERT).

CHAIN PRECURSOR

NI-O9. KUS MOSCULUS (MOUSE). EUKARYOTA: KETAKOA: CHORDATA: VERTEBRATA: TETRAPODA; MAMMALIA: EUTHERIA: RODENTIA.

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7: DB 1: Length 199; Pred. No. 5.98e+00; O; Mismatches O; Indels

9

Gaps

0

INIT_MET U V V 0426BB63 CRC32;

MICHO MAT. STANDARD; PRT: 199 AA.
101-A0G-1990 (REL. 15, CREATED)
01-A0G-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-A0G-1990 (REL. 15, LAST ANNOTATION UPDATE)
101-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
101-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
110-1996 (REL. 13, LON-TWITCH KUSCLE B/VENTRICULAR ISOFORM.
1110-1996 (REL)
110-1996 (SEQUENCE FROM N.A.
TISSUE-HEART VENTRICLE;
HEDLINE, 89240011.
HCUALLY E. BUTTRICK P., LEINAND L.;
NUCLEIC ACIDS RES. 17:2753-2767(1989).

EQUENCE FROM N.A. STRAIN-WISTAR; TISSUE-HEART VENTRICLE; SEDLINE; 90016857.

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STATETARRE HSSP: P01899; INCC.

MGD: MGI: 95938; HZ-Q9.

PROSITE: P800290; IG_MHC: PAR:

MHC I; GLYCOPROTEIN; SIGNAL.

SIGNAL 21 >200 PARTIAL.

DOMAIN DOMAIN DISULFID CARBOHTD NON_TER SEQUENCE

461493EE CRC32;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 200; Pred. No. 5.98e+00; 0; Nismatches 0; Indels 0 Caps

97 GSLRTAQ 103 ||||||| 1116 GSLRTAQ 1122

STANDARD; PRT;

COPLASMA PREDMORIAE. NORANTOTA: TENERICUTES; MOLLICUTES; MYCOPLASMA; MYCOPLASMATALES; COPLASMATACEAE.

US-08-951-733-20.rsp

22 > 112 > 107 200 A, 111 2 200 22 185 20 107 20 2005 MW: 4 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, OP ALPHA CIRLH:
EXTRACELUTIAR ALPHA-1.
EXTRACELUTIAR ALPHA-2.
BY EMILARITY.
POTENTIAL.

TLT 23
DEF_MTCPN
P75527:
01-NOV-1997 (1
01-NOV-1997 (1
01-NOV-1997 (1
01-NOV-1997 DPF
POLYPEPTIDE DE
DEFORMYLASE). (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)

A RINGELEC FROM N.A.

STRAIN-ARCC 29342 / H129:

X MEDLINE; 9105885.
A HIMBELRECK R., HLERET H., PLAGENS H., PIRKL B., LI B.-C.,
A HERROMAN R.

L NUCLEIC ACIDS RES. 24:4420-4449(1996).
C HERROLE SENS. 24:4420-4449(1996).
C C-CALALTIC ACTIVITY: N-PORNIT-L-MEDHIONIE + H(2)0 = FORMATE +
C C-CALAUTIC ACTIVITY: N-PORNIT-L-MEDHIONIE + H(2)0 = FORMATE +
CC C-COPACTOR: REGULIES AND BIND A EINC 109 (BY SIMILARITY).
DR ENGL. ACCOUNT: NONDER (BY SIMILARITY).
DR ENGL. ACCOUNT: MONDER (BY SIMILARITY).
DR ENGL. ACCOUNT: MONDER (BY SIMILARITY).
FIN PROTEIN BIOSYMPHSEIS; HIDDALASE; EINC.
FIN METAL 178 178 XINC (BY SIMILARITY).

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1998

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Page

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SENCIANCE FROM N.A.
STRAIN-CSTRAID;
STRAIN-CSTRAID;
BETLIN J.J., PAULSON H., FLAVELL R.A.;
BETLIN J.J., PAULSON B., FRAVELL R.A.;
BENG J. 4.3203-3207(1985).
1- PERINTION: INFOLVED LET THE PRESENTATION OF FOREIGN ANTIGENS TO
1- SERVICIANTEMEN OF ALPHA CHAIN AND A BETA CHAIN (BETA-2EMBL; NO3443), GSB2404; ALPHA CHAIN AND A BETA CHAIN (BETA-2EMBL; NO3443), GSB2404; ALPIA CHAIN AND A BETA CHAIN (BETA-2-

FT ACT_SITE 179
FT METAL 182
SQ SEQUENCE 216 AA; 179 B1 182 E: 24592 MW; BY SIMILARITY. SINC (BY SIMILARITY). ; 8ED05092 CRC32;

Query Match 0.81, Scorre 7; DB 1; Length 216; Best Local Similarity 100.01; Pred. No. 5, 98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0; Indels ္ပ Gaps

0

208 NPALPSD 214 ||||||| 1142 NPALPSD 1148

TEGL_CAZEL STANDARD: PRT: 257 AA.

TEGL_CAZEL STANDARD: PRT: 257 AA.

P55336; Q19405;

Q1-cCT-1996 (REL. 34, CREATED)

Q1-cCT-1996 (REL. 34, LAST SEQUENCE UPDATE)

Q1-wor-1997 (REL. 35, LAST ANDOVATION UPDATE)

HTPOTHETICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X.

#13E6.1. CAENORHABDITIS ELEGANS. EURANYOTA; KETAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA

ENDITECT FROM N.A.
STRAIN-BRISTON, N.;
STRAIN-BRISTON, N.;
HAGCERIGON 9., 195) TO EMBL/GENBANK/DIBJ DATA BANKS.
SUBMITTED (MOV.) 195) TO EMBL/GENBANK/DIBJ DATA BANKS.
L. SERLABITT. TO HOMAN PROTEIN D52.
EMBL, SERIOJS, CED1198.
HTMONUMERICAL, PROTEIN D52.
SEQUENCE 257 AA; 26696 MH; 66FDB900 CRC32;

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 1; Length 257; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0 Caps 9

30 DAVVIEQ 36 |||||| 810 DAVVIEQ 816

US-08-951-733-20.rsp

R PERLIANNY M. MOCAGNINAR, KUNARC, MARTIN B.J., SIDDIQUI M.A.Q.;
RU MUCLEC, M.C. 1258 285. 17723-7734 (1985)
CC -1- SMIRINT; MOSIN 15 M. BEXAMER OF 2 REAVY CHANGE & 4 LICHT CHAIRS.
CC -1- SMIRINT; MOSIN 15 M. BEXAMER OF 2 REAVY CHANGE, BUT THIS
CC -1- SMIRINT; MOSIN 15 M. BEXAMER OF 2 REAVY CHANGE, BUT THIS
CC -1- SMIRINT; MOSIN 15 M. BEXAMER OF 2 REAVY CHANGE, BUT THIS
CC -1- SMIRINT; MOSIN 15 M. BEXAMER OF 2 REAVY CHANGE; BUT THIS
CC -1- SMIRINT; MISSIS OF 3 MIND CALCIUM.

REASI: MISSIS COSSIS; -CR ESSI: MISSIS PROTEIN; MULTICEME FAMILY.

FT HITLMET O 0

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TAKAHASHI

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RESULT 26

TEPA_HUMAN STANDARD; PRT; 278 AA.

TO P1958; PSG (REL. 33, CREATED)

TO 1.PES-1996 (REL. 33, LAST SECUENCE UPDATE)

TO 1.PES-1996 (REL. 34, LAST SECUENCE UPDATE)

TO 1.PCT-1996 (REL. 34, LAST SECUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE STATES OF THE STATES
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ON PROTEIN, ARE PRODUCTS OF THREE DIFFERENT MERAS SPLICED FROM THE SAME PROJECTS.

SAME PRIMATURY PRODUCTS OF THREE DIFFERENT MERAS SPLICED FROM THE ELA REGION OF THE GENOME.

RESUL AND CORSES.

RESUL ADSOLOGISSIS.

R
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                     -: SUBCELLULAR LOCATION:
-: SUBCELLULARITY: BELONGS T
PROTEINS.
EMBL: L11577: G310632: -
TRANSLEMBRANE: TRANSPORT.
TRANSLEMB 18 98
TRANSMEM 40 60
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STRAIN-GOMEN; 91237792.
MEDIJKERA R., DEKKER B.M.M., V
DOTKER H.W.;
GENE 12:287-299(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 LLCSLCY 184
||||||||
862 LLCSLCY 868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMOURICE FROM N.A.
STRAIN-PEA68.
MEDILINE: 95012638.
KOLENBANDER P.E., ANDERSEN R.N., GAMESHKUMAR N.;
INFECT. IMPUN: 62:4469-4480(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROMO SADIENS (UDMAN)
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRIDAE; DS-DNA NONENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09:28:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
S TO THE ABC-3 SUBPAMILY OF INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7; DB 1; Length 261;
Pred. No. 5.98+00;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADENOVIRIDAE; MASTADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-951-733-20.rsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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REGUIT 27

ID P391 SIRGC STANDARD; PRT: 278 MA.

AD 101-80V-1995 (REL. 37 CREATED)

DT 01-80V-1995 (REL. 32 LAST SECURING UPDATE)

DT 01-80V-1995 (REL. 33 LAST SECURING UPDATE)

DT 01-80V-1995 (REL. 33 LAST SECURING UPDATE)

DT 01-80V-1995 (REL. 31 LAST SECURING UPDATE)

OS STREPTOCCCUS GORDONIC CHALLS.

OS PROMANION, FIRMICUTES; COCCI; STREPTOCCCCARAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                            片
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RP VARIANT AVED GLH-101.

RP VARIANT AVED GLH-101.

RP VARIANT AVED GLH-101.

RA CODDLINE: 960266.

REPARATE MENDEAUSE.

CC -1 FUNCTION: BIUSA ALDRA-TOCOPHEROL AND ENHANCES ITS TRANSPER BETWEEN GREEN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.8; Score 7, DB 1; Length 278;
Best Local Similarity 100.0; Pead No. 5:98e+00; Indels
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                  36 REAGVPL 42
|||||||
230 REAGVPL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
DENG H.X., HENTATI A., SIDDIQUE T.;
SIBMITTED (FEB-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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278 AA:
                                            Score 7; DB 1; Length 278;
Pred. No. 5.98e+00;
O; Mismatches 0; Indels
                            POTENTIAL
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 indels
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Gaps
  0
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                                                     Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
232 GASVLGL 238
||||||||
699 GASVLGL 705
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RL	3	3	3	3	3	Z	æ	2	8	8	S	e G	ğ	ដ	3	3	č	ä	RESULT
DNA RES. 3:109-136(1996).	YAMADA M., YASUDA M., TABATA S.;	OXUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,	HOSOUCHI T., MATSUNO A., MURAKI A., MAKAZAKI M., MARUO K.,	MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,	KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,	MEDLINE: 97061201.	SEQUENCE FROM N.A.	[1]	CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES.	PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;	SYMECHOCYSTIS SP. (STRAIN PCC 6803).	DNAJ OR SLL1933.	DNAJ PROTEIN.	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)	01-MOV-1997 (REL. 35, CREATED)	P73097;	DNAJ_SYNY3 STANDARD; PRT; 307 AA.	CT 28

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ALT THE PRICE LAMEDA COLOR OF REPLICATION AND TO SUMMANDRIE A PROTEIN COMPLEX WITH GROSE, THE APPACE ACTIVITY OF DAMA. (BY SIMILARITY).

1- SHILLARITY. TO CHESS PROMATOTIC DAMA, AND TO SUMARTOTIC DAMA-LIZE PROTEINS.

2014. D80030, 01851188.

PROSETTS. PSS0076: DAMA-2; 1.

PROSETTS. PSS0076: DAMA-2; 1. DOMAIN 89 110 GLY-RICH. SEQUENCE 307 AA; 34698 MW; 5E785CAD CRC32;

Query Match

Best Local Similarity 100.0%;
Matches 7; Conservative 129 VVSPARP 135 ||||||| 294 VVSPARP 300 Score 7; DB 1; Length 307; Pred. No. 5.98e+00; 0; Mismatches 0; Indels Indels 0 Caps 0

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SAPE_POOLI SAPE_POOLI 9/1621; POIL 9/1621

SEQUENCE FROM N.A. STRAIN-K12 / FRAG5; EPSTEIN W., NOELKER E., SUBMITTED (APR-1996) TO SECHERICHIA COLI. PROMANTOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY AMAEROBIC RODS; EMPEROBACTERIACEAE:

STOMPE S., TEWES R., SCHMID R., EMBL/GENBANK/DDBJ DATA BANKS.

BAKKER

SEPCIENCE FROM N.A. STRAIN-RIZ / MC1655; BLATMER F.R., PLUNNETT G. III, MAYHEM G.F., PERNA N.T., GLASNER F.D.: BUNTTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

SENCHMEND FROM N.A.
SENAIM-KILLS FROM N.A.
AIDA H., BARA T., FULTA K., HAYASHI K., HONJO A., HORITOHI T.,
AIDA H., BARA T., JEONO K., ISONO S., ITOH T., KANI K., HAKINO K.,
IKAMOTO K., INIM T., ISONO K., ISONO S., ITOH T., KANIKA K., HAKINO K.,
MASHADTO K., HISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
NASHADTO H., HISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
NASHADTO H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO K.;

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SUBHITTED (DEC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

- FUNCTION: INVOLVED IN A PEFFIDE INVAKE TRANSPORT SYSTEM THAT

- PLAYS A ROLE IN THE RESIGNACE FOR ANYILICADOLL PEPTIDES.

- SUBCELUTAR LOCATION: INTEGRAL MEMBRANE PROTEIN: INNER MEMBRANE (POTENTAL).

SINILARIT: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE OPPBC SUBPANILY. PALSE_NEG.
RANE; INNER MEMBRANE

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7: DB 1; Length 321; Pred. No. 5.98e+00; 0; Mismatches 0; Indels 0; Caps

83 LAFGFAL 89 ||||||| 119 LAFGFAL 125

LT 30

SADS_SALTY STANDARD; PRT; 321 AA.

P35668;
01.-70F-1994 (REL. 29, CREATED)
01.-70F-1994 (REL. 29, LAST SEQUENCE UPDATE)
01.FEF-1995 (REL. 31, LAST ANDOVATION UPDATE)
PERTIDE TRANSPORT SYSTEM PERMEASE PROTEIN SAPB.

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287 ASRSLPL 293 ||||||| 250 ASRSLPL 256

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JÜNDERGE FROM N.A.
JÜNDLIKE: 94038887.
KEDLIKE: 94038887. N.T., GROISMAN E.A.;
KARA-LODEE C., BARE N.T., GROISMAN E.A.;
KEBO J. 12:4053-4063(1993).
                                                               LOGIELLA TYPHIMURUM.
DYARYOTA: GRACILIGUTES: SCOTOBACTERIA; PAGULTATIVELY AMAEROBIC RODS
TREDBACTERIACEAE.
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Best Local Similarity 100.0%;
Matches 7; Conservative
overy Match 0.6%; Score 7; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 5.98++09;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 LAFGFAL 89
||||||
119 LAFGFAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSPORT: PEPTIDE TRANSPORT: 7
TRANSPORT: PEPTIDE TRANSPORT: 7
TRANSPER | 11 | 11 | 10 |
TRANSPER | 11 | 11 | 10 |
TRANSPER | 17 | 11 | 10 |
TRANSPER | 17 | 10 |
TRANSPER | 17 | 10 |
TRANSPER | 17 | 10 |
TRANSPER | 31 | 10 |
TRANSPER | 31 | 10 |
TRANSPER | 31 | 10 |
TRANSPER | 31 | 10 |
TRANSPER | 31 |
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EMBL: X74312; G414209; -.
PIR: S39586; S39586.
STYGENE: SG10378; SAPB.
PROSITE: PS00402; BPD_TRANS
                                                                                                                                                                                                                                                                                                                 CENTLES 6. CHURCHER C.M., BARRELL B.G., RAJANDREM K.A., WALSH S.V.;
SUBMITTED (UL.1995) TO SEBL/GEBRANK/DDSD DATA BANKS.
1- SHALARITY: STRONG, TO PAST THROSSC.
EMBL. SEOL43: 01053799; T. PAST THROSSC.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAZE_SCHPO STANDARD; PRT; 329 AA.
090704;
01-W0V-1995 (REL. 32, CREATED)
01-W0V-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-W0V-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-W0V-1995 (REL. 32, LAST ANOPATION UPDATE)
HTPOTHERICAL 56.7 ND PROTEIN C2F7.14C IN CHROMOSOME
SPACEF7.14C.
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EUKANYOTA; FUNGI; ASCONYCOTINA; HEMIASCONYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-972;
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SEBCELLILAR LOCATION: INTEGRAL MEMBRARE PROTEIN. INNER MEMBRARE
(POTENTIAL).
SIMILARITY: MITH INTEGRAL MEMBRARE CONFORMETS OF OTHER BINDING-
PROTEIN DEPENDENT TRANSPORT SISTEMS. BELONGS TO THE OPPBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13300.
13300.
131 BOLTHANSP_INI_MEMOR: FLISE_NEG.
131 BOLTHANSPORT; TRANSMEMORANE; INVER MEMORANE.
132 POTENTIAL.
133 POTENTIAL.
134 POTENTIAL.
135 POTENTIAL.
147 259 POTENTIAL.
149 259 POTENTIAL.
149 259 POTENTIAL.
150 POTENTIAL.
151 AN; 36083 MF; 02817BFO CRC32;
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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RECURRE OF 292-334 FROM N.A.

REPENDINE; 91063111.

RA HEDLINE; 91063111.

REPENDINE OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-LICENTROLLE)

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NANCKK G.L. SERBMAN D.H., CALVIN S., ALLEN H., FLAVELL R.A.;
J. EXP. MED. 165:1358-1370(1997). STRAIN-C5781/10: MEDILHE: 66135949. DEVLIN J.J., WEISS E.H., PAULSON M., FLAVELL R.A.; EMBO J. 4:3203-3207(1985). EROMENCE PROM N.A.
EROMENTE M. PRELINCER J.G.,
STEINWEITE M., MOORE K.W., PRELINCER J.G.,
BOTSE E.A., EROD L.;
LELL 25:683-692(1981). SHER B.T., SHEN F.W., 경

TOSA_SCHOO STANDARD; PRT; 330 AA.

Q10114;
Q10114;
Q10114;
Q10114;
Q10107 (REL. 14, CERATED)
Q1-cort_1996 (REL. 14, CARE REGURENCE INDATE);
Q1-cort_1997 (REL. 15; CAST ANNOTATION UNDATE);
Q1-cort_1997 (REL. 15; CAST ANNOTA

Query Match 0.6%; Score 7; DB 1; Length 330; Best Local Similarity 100.0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels

0 Gaps B

SOUTHING FROM N.A. SARRELL B.G., RAJANDREAM M.A., WALSH S.V., DEVILLE N.G., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V., DEVILLE N.G., CHURCHER S.V., DEVILLE N.G., CHURCHER S.V., CHURCHER

220 QLLRQHS 226 ||||||| 472 QLLRQHS 478

Query Match 0.6%; Score 7; DB 1; Length 334;

Page 52

H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, OF ALPHA CERLY: EXTRACELUTIAR ALPHA-1. EXTRACELUTIAR ALPHA-2. EXTRACELUTIAR ALPHA-3. CONNECTING PEPTIDE.

RP 4 C E E STORY

MUS MUSCULUS (MOUSE). BURARYOTA, HETAMOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMGALIA; EVYHERIA; RODENTIA.

BAIT JOOSE STANDARD: PRT: 334 AA.
P14439:
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, CREATED)
01-ROV-1997 (REL. 15, LAST ANDOTATION UPDATE)
H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, 07 ALPHA
(QA-2 ANTIGEN).

SEQUENCE PROM N.A.

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Best Local Similarity 100.0%; Pred. No. 5.98e+00; Matches 7; Conservative 0; Mismatches 0; Indels 0;

Gaps

0

ş 8

97 GSLRTAQ 103 ||||||| 1116 GSLRTAQ 1122

SELUT 14.

PATOS. 19.6 (REL. 31, GREATED)

10. FEB. 19.6 (REL. 31, GREATED)

10. FEB. 19.6 (REL. 31, LAST SEQUENCE UPDATE)

10. CCT. 19.6 (REL. 31, LAST ANNOVATION UPDATE)

10. CCT. 19.6 (REL. 31, LAST ANNOVATION UPDATE)

PETILO PROTEIN

RESULTANT DE LA COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPANIA DEL COMPANIA DE

SEQUENCE FROM N.A.

CUI I., MASON T.;

CUI II., MASON T.;

CUNITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

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BY STRAILER, JANCE 39145;

BR MEDIJER, 4459160.

BR MEDIJER, 4459160.

CO -1- CATALTIC ACTIVITY: UDP-GLICCOSE = UDP-GALACTOSE.

CO -1- CATALTIC ACTIVITY: UDP-GLICCOSE = UDP-GALACTOSE.

CO -1- CATALTIC ACTIVITY: UDP-GLICCOSE = UDP-GALACTOSE.

CO -1- PATHWALTY. EXPODULSANCHARIDE AND LIPOPOLYSANCHARIDE BIOSYNTHETIC CO: -1- PATHWALTY. NITH OTHER GALACTOWALDENASES FROM EUKANYOTIC AND COMPANIOTIC ORGANICATION OF COMPANION OF COM
REPORTED FROM N.A.

REPORTED 1.

REPORTED 2.

REPORTED 3.

REPORTED 4.

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Best Local Similarity 100.0%;
Matches 7; Conservative
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Matches 7; Conservative
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1104 LTRHRVT 1110
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SEQUENCE
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247 GGSASRS 253
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TIA, PASIT STANDARD; PRT; 355 AA.
P21109;
01-PMT-1991 (REL. 17, CREATED)
01-PMT-1992 (REL. 25, LAST RESOURCE UPDATE)
01-WMT-1992 (REL. 25, LAST RESOURCE UPDATE)
01-WMT-1997 (REL. 25, LAST RESOURCE UPDATE)
11-REA APETIMITY HITERLEVATIN-8 RECEPTOR A (II-8R A) (CXCR-1).
11-REA APETIMITY HITERLEVATIN-9 RECEPTOR A (II-8R A) (CXCR-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PREZ_HUMAN STANDARD; PRT; 356 AA.

PA115;

PA115;

PA115;

PA115;

PA115;

PA115;

PA115;

PA116;

PA1
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TISSUE-PLACENTA:
MEDILHE: 94394817 T.J., PEPPERL D.J., PIERCE K.L., BOCARDUS A.H.,
REGAN J.W., BAIREY T.J., PEPPERL D.J., FIERCE K.L., BOCARDUS A.H.,
DOMELLO J.E., FAIRBAIRN C.E., KEDZIE K.H., WOODWARD D.F., GIL D.W.;
MOL. PHARMACOL, 46:213-220(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEOSPIRILLUM BRASILENSE.
PLASHID MEGAPLASHID P90.
PROKANYON, GRACILLOTUES: SCOTOBACTERIA;
AEROBIC, MOTILE, HELICAL AND/OR VIBRIOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

REDLINE: 9178994.

BECHMAN M.P., HONGER W.E., KOZLOSKY C., VANDENBOS T., PRICE V.,

ITANA S., CERAD N.P., GERAND C., CERNETTI D.P.;

BICCHEM. BIOPRIS. RES. COMMUN. 179:784-789(1991).
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STRAIN=ALBINO; TISSUE=NEUTROPHILS;
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204
287
355 AA;
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204 R
288 D)
40622 MW;
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R -> C (IN REF. 2).

DI -> EL (IN REF. 2).

M: 2EB3947D CRC32;
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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RESULT PAC QUAN PAC Q

PRT: 348 AA.
Q\$903;
O1:ROV-1997 (REL. 35, CREATED)
O1:ROV-1997 (REL. 35, LAST ESQUENCE UPDATE)
O1:ROV-1997 (REL. 35, LAST ESQUENCE UPDATE)
O1:ROV-1997 (REL. 35, LAST SAUGUENCE UPDATE)
UDP-GLICCOSE 4-EPIMERASE (EC 5.1.3.2) (UDP-GALACTOSE 4-EPIMERASE)

Overy Match 0.6%; Score 7; DB 1; Length 347; Best Local Similarity 100 0%; Pred. No. 5.98e+00; Indels Matches 7; Conservative 0; Mismatches 0; Indels

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Gaps

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MITOCHONDRION. SEQUENCE 347 AA; 39812 MW; 85A9097F CRC32;

SEQUENCE FROM N.A.

PORL T.M., ALINOVIC G.;

PORLT.TM., TALINOVIC G.;

PORLT. TM., TALINOVIC G.;

PORLT. GEP. 1999 G. DEBLYGENBANK, DEBJ DATA BANKS.

1- FUNCTION: HOT KNOW, PET130 NUTANTS ARE DEFICIENT IN HITOCHONDRIAL

PROTECTIN SYNTHESIS.

1- SUBJECTION STATEMENT OF THE STATE

67 STLIDLQ 73 ||||||||| |786 STLIDLQ 792

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MEDLINE: 91056034.
THOMAS K.M., PTUN H.Y., NAVARRO J.;
J. BIOL. CHEM. 265:20061-20064(1990)
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EQUENCE FROM N.A.

LEE J. KUANG W.-J., RICE G.C., WOOD W.I.;

LEE J. KUANG W.-J., RICE G.C., WOOD W.I.;

J. MONDOL. 148:126:-1264(1992).

1- FUNCTION: RECEPTOR TO INTERLEURIN-8, WHICH IS A DOWERFUL.

1- FUNCTION: RECEPTOR TO INTERLEURIN-8, WHICH IS A DOWERFUL RECEPTOR RECEPTOR PROTECTION FOR THE RECEPTOR OF IL-8 TO THE RECEPTOR OF IL-8

3Y SIMILARITY. DLLFALTMPIWAYSKEKGWIPG -> PAFCPDHAYLGRLQGKRLDPR (IN REF. 2).

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US-08-951-733-20.xap
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Page 57
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US-08-951-733-20.rsp
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Page 58
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DI TERE JUNAN STANDARD, PRT. 375 AA.

C 999712 (19446) 609564
7 01-NOV-1997 (REL. 35, CREATED)
77 01-NOV-1997 (REL. 35, CREATED)
77 15-JUL-1998 (REL. 36, LAST ANNOTATE)
78 101-SENSITIVE INPADE RECTIFIER FORMSON OFDATE)
82 CHARREL, HRARDLY RECTIFIER, SUBPANILY J, HEMBER 15) (INFARD BECTIFIER FORMSON OF SUBPANILY J, HEMBER 15) (INFARD BECTIFIER SUBPANILY J, HEMBER 15) (INFARD BECTIFIER SUBPANILY J)
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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1- PRINTENT REACTION OF GALACTOSE METHNOLISM (LEIGHE PATHWAY).
1- SHALLARITY. TO CTHER PROMATEOUT AND ENTANTONISMESS.
1- CANTION: REF. 1 ROUGHES FORM THAT SHORE IN POSITIONS 49
10 51, 181 TO 244, AND 28 TO 310 DE TO PRAMESHIPTS.
10 51, 181 TO 244, AND 28 TO 310 DE TO PRAMESHIPTS.
10 181 TO 244, AND 28 TO 310 DE TO PRAMESHIPTS.
12 181 TO 244, AND 28 TO 310 DE TO PRAMESHIPTS.
12 181 CALACTOKINASE. 1.
12 181 TANSES GALACTOKINASE. 1.
13 APPOPULICE: AND PRINTIAL.
14 19 63 ALPOPOPULISH: AND-BINDING.
15 ALPOPOPULISH: AND-BINDING.
16 18 ALPOPOPULISH: AND-BINDING.
17 ALPOPOPULISH: AND-BINDING.
18 BIND 12 13 ALPOPOMAYSBREER. -> DERTHERBEDSDOANDG
18 COMPLICT 49 63 (1M REF. 1)
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-- CATALYTIC ACTIVITY: ATP + D-GALACTOSE = ADP + D-GALACTOSE
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AEDLINE: 8006669.
UDANS C.M., FORMANIO J.A., SCHWIDT F.J., ROSENBERG M., BRANNER M.E.;
DACTERIOL. 170:203-212(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPTONYCES LIVIDANS.
OKARYOTA; FIRMICUTES; ACTINONYCETALES; STREPTONYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AN-1990 (REL. 13. GREATED)
-NOV-1995 (REL. 32. LAST SEQUENCE UPDATE)
-NOV-1995 (REL. 32. LAST ANNOTATION UPDATE)
LACTORINASE (EC 2.7.1.6).
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SSUE-KINNEY,
SUENTINEY,
UCR M.E., PISSET A.M., BOCK J.H., SLIGHTON J.L.,
BIOL. CHEM. 271:586-593(1997).
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Pred. No. 5.98e+00;
O; Mismatches 0; Indels
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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65555569 CRC32;
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-> R (IN REF. 2).
8EF7D003 CRC32;
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(TRACELLULAR (POTENTIAL).
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Best Local Similarity 100.0%;
Matches 7; Conservative
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P02465;
21-JUL-1986
21-JUL-1986
01-NOV-1995
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|||||||
804 ETSPLRD 810
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MEDLINE: 76091874.
PTETER P.P., REXROOT F.W.;
EUR. J. BIOCHEM. 59:113-118(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SENDURKCE OF 1-19.
MEDLINE: 75036115.
FIETEER P.P., BREITKREUTE D., KUEHN K.;
FIETEER P.P., BREITKREUTE D., KUEHN K.;
FICHOLIN. BIOPEYS. ACTA 365:305-310(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOS TANBUS (BOVINE).
EULANYOTA, METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMALIA;
EUTHERIA; ARTIODACTULA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIETZEK P.P., FURTHWARR H., KUZHN K.;
EUR. J. BIOCHEM. 47:257-261(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 337-366.
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ISSUPAKIDER;
MTORI M., SEKI N., NACASE T., SUZUKI E., NOMURA N., OHARA O.,
MTORI M., SAKAKI Y., EKI T., MURAKAHI Y., SAITO T., ICHIKAWA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TL-1986 (REL. 01, CREATED)
TL-1986 (REL. 01, LAST SEQUENCE UPDATE)
VV-1995 (REL. 32, LAST ANNOTATION UPDATE)
VGEN ALPHA 2(I) CHAIN (FRACKENT).
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235
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375 AA;
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 7; Conservative
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P06739;
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MEPA_MOSE STANDARD: PRT: 420 AA.
P81171
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST ANDOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANDOTATION UPDATE)
DAN-BINDING PROTEIN NEPA PRECURSOR.
MEPA.
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1079 GAKGAAG 1085
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STRAINSHESS RESERVE / NIH: TISSUE-EMBRYO!

HORFIG K. BARNIGOL-WAYNANDE S., BARNIKOL U., HILSCHANN N.;

SUBMITTED (NOV.1997) TO SEBL/CERBINK/DBN DAYA BANKS.

1- FUNCTION: HAS A DNA BINDING PROPERTY. THE POTEWILK HE FLAND

1- FUNCTION: HAS A DNA BINDING FROPERTY. THE POTEMIKE THE

DNA-BINDING FUNCTION OF THE PROTEIN OF MY REGULATE THE

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1- SEPLETIONAR LOCATION: SECRETED (POTEMIAL).

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1- STREELITIAR LOCATION: SECRETED (POTEMIAL).
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NON_TER 402
SEQUENCE 402 AA;
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BULANYOTA, METALOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DÉURMES PROM M. B.
TRAINS-288C , DAPT:
TRAINS-288C , DAPT:
DOINS-700 M. ANDREWS S., BRINDAN R., COOPER J., DING R., DOVER J.,
DOINS-700 M., ANDREWS S., BRINDAN R., COOPER J.,
DOINS-700 M., ANDREWS S., BRINDAN R., CEISEL C., RISSTAN J.,
TÜCAN T., HILLER L., JURE M., JOHNSTON L., LANGENSON F.,
HORDING P., LOUIS R.J., MACHAN M., MERZHA L., RICKEL M., RICKLE M., RI
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11. FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
11. -CC-1996 (REL. 34, LAST SEQUENCE UPDATE)
11. -CC-1996 (REL. 34, LAST SEQUENCE UPDATE)
11. FORTIETICAL 51.1 KD PROTEIN IN DCD1-NRP16 INTERGENIC
1R1.469.
                                                                                                                                                                                                ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
IARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                           CHERICHIA COLI.
SAND PHIYISZ.
Maryota, gracilicutes, scotobacteria, facultatively amaerobic rods
Terobacteriaceae.
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25 POTENTIAL.

26 DA SINGIA PROTEIN HEFA.

27 BY STRILARITY.

28 STRILARITY.

29 BY STRILARITY SIGNAL (P. 114)

20 HUCLERR LOCALIZATION SIGNAL (P. 114)

214 SUCLER (POTENTIAL).

25 SIZE 1 (POTENTIAL).

26 LECCIDE 2 (POTENTIAL).

37 LECCIDE 2 (POTENTIAL).

38 LECCIDE 2 (POTENTIAL).
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402
36257 MW; 3Flacaze CRC32;
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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Pred. No. 5.98e+00;
0; Mismatches 0; Indels
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                RESULT 45

DENTIFY ACOLI STANDARD; PRT; 478 AA. AC P0986;

DT 01-MAR-1989 (REL. 10, CREATED)

DT 01-MAR-1989 (REL. 11, LAST SEQUENCE UPDATE)

DT 01-MAR-1989 (REL. 13, LAST SEQUENCE UPDATE)

DT 01-CAT-1986 (REL. 13, LAST SEQUENCE UPDATE)

DE REMOLIZIS SECRETION PROTEIN D, CHROMOSONAL.

GN HITD.

OS SECRETION COLLICOTES; SCOTOBACTERIA; PACULTAT

RN 121-CATE FROM HA.

RN PELMIRES FOR THE 04;

RN REDLIES 5531404.

RN REDLIES 5531404.

RN 121-CATE SON THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mon
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A SCHPELEN, P. GERTSCHEY I., MOLLENROPF H.-J., GOEBEL W.;

LM. MOL. GER. GERET. 234.155-163(292).

CO. 1- FUNCTION: INVOLVED IN THE TRANSPORT OF HEMOLYSIN A.

CO. 1- FUNCTION: INVOLVED IN THE TRANSPORT OF MEMOLYSIN A.

CO. 1- FUNCTION: INVOLVED IN THE TRANSPORT OF MEMOLYSIN PROTEINS.

CO. 1- FUNCTION: INVOLVED IN THE RESEARCH PROTEINS.

CO. 1- FUNCTION: INVOLVED IN THE HILD PARTILL OF MEMOLYSIS FOR PROSECULATION FROM THE MEMOLYSIS FUNCTION FOR THE MEMOLYSIS FUNCTION FUNCTION FOR THE MEMOLYSIS FUNCTION FUNC
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Matches 7; Conservative
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|133 TLTALEA 1139
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RES. MICHOSIDI. 141:336-341(1990).

RES. MICHOSIDI. 1700LYED IN AREBRICAL RESISTANCE. THOOGHT TO PORM THE CHANKEL OF AN AREBLITE POUR.

1- SUBCELLILAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE PROTEIN. JOSES 1.

PORRABLED. 151:1858; ...

PIR. BESSOT: BESSOT: TANNSHEMBRANE: INNER MEMBRANE.

PLASHID. AREBRICAL RESISTANCE: TRANSHEMBRANE: INNER MEMBRANE.

BEOGRECE 429 AM; 45558 MM; 7DFFEMB; CRC12;

BEOGRECE 429 AM; 45558 MM; 7DFFEMB; LEAGTH 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 KRAERLT 218
|||||||
671 KRAERLT 677
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|||||||
1058 ISDTASL 1064
TOPOLOGY.
MEDLINE: 92357011.
SCHUELEIN R., GENTSCHEV I., MOLLENKOPF H.-J., GOEBEL W.;
                                                                                                                                                                                                                                                                                                                                                                                     SEGIERICHIA COLI.
PROMANYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
ENTENDENCIPRIACEAE.
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HESS J., WELS W., VOGEL M., GOEBEL W.;
FEMS MICROBIOL. LETT. 34:1-11(1986).
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Pred. No. 5.98e+00;
0; Mismatches 0; In
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0; Mismatches 0;
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Pred. No. 5.98e+00;
O; Mismatches 0; Indels
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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative

Score 7; DB 1; Length 479; Pred. No. 5.98e+00; 0; Mismatches 0; Indels

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Caps 9

0

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RESSUZA 46

IN OPRA JESALE STANDARD; PRT; 479 AA.

AC 051397; REL. 35, CREATED;
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE);
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE);
DT 01-NOV-1997 (REL. 35, LAST ANNOVATION OFFI ANNOVATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S (1)

P SEQUENCE FROM N.A.

C STRAIN-PAD;

A PROGLE K., GOYDE N., TEUTINOTO H., ERAO Q., WADA A., TAMASAKI T.,

A RESHAT S., YAMAGISHI J., NISHIGO T.)

AL SURMITED, CULL.1995 TO DEBLACERAMK, DEBU DATA BANKS.

CC. I- FUNCTION: CHANNEL-FORMING COMPONENT OF A MULTIDROG RESISTANCE

CC. I- SURGELLULAR LOCATION: ATTACHED TO THE OUTER MEMBANE BY A LIPID

CC. I- SURLIARITY: BELONGS TO THE FUSA, MODY FAMILY.

CC. I- SINLIARITY: BELONGS TO THE FUSA, MODY FAMILY.

DR PROSITE: PSOID(13) PROGRAL, LIPOPROTEIN; LIPOPROTEIN; SIGNAL.

EN CUTER MEMBANE, ANTHEONY C RESTANCE; LIPOPROTEIN; SIGNAL.

FT SIGNAL 1 19 BY SHILARITY.

FT SIGNAL 20 479 AN: $1973 MM; ASTECONC CRC32:

FT CHAIN 20 479 AN: $1973 MM; ASTECONC CRC32:
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# SEQUENCE PROM N.

# PEDUTHE: 8977-32717PLE M.A., DAVISON A.J., DOLAN A., FRAME M.C.,
# MEDICHE: 8977-32717PLE M.A., DAVISON A.J., DOLAN A., FRAME M.C.,
# MEDICHE: 8971-32717PLE M.A., DAVISON A.J., DOLAN A., FRAME M.C.,
# MEDICHE: 8971-3271 | SCOTT J. E., TANICOR P.,
# COURTED | SOLIT | SOLIT | SOLIT | SOLIT | SOLIT |
# PEDICH: MAD | SOLIT | SOLIT | SOLIT | SOLIT |
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C --- PROCITON: INCLUDED IN THE TRANSPORT OF HEMOLITSIN A.

C --- SUBCELLULAR LOCATION: INMER HEMBRARE-BOUND (POTENTIAL).

C --- SIMILARITI: ENCORES TO THE HLTD PANIL! OF SECRETION PROTEINS.

PERI: MOIST: PEROSA: HLTD PANIL! OF SECRETION PROTEINS.

PERI: PASSED: HLTD PANIL! INVESTMENT FOR PROSITE: PROSA1: TOPPASSED PANE: INNER MEMBRANE.

PROMAIN: 10 10 10 POTENTIAL).

PROMAIN: 61 478 PREIPLASMIC (POTENTIAL).

PROMAIN: 81 478 PREIPLASMIC (POTENTIAL).

SOURCE 478 AA: 54591 MM; 721A007E CRC3;
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Best Local Similarity 100 0%; Pred. No. 5. 98e+09;
Matches 7; Conservative 0; Hismatches 0; Indels
overy Match 0.6%; Score 7; DB 1; Length 535;
Best Local Similarity 100.0%; Pred. No. 5.98e+00;
Matches 7; Conservative 0; Mismatches 0; Indels
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717 LRVRAGD 723
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P09855;
Ol-MAR-1999 (REL. 10, CREATED)
Ol-MAR-1999 (REL. 10, LAST SEGUENCE UPDATE)
Ol-DEC-1992 (REL. 24, LAST ANNOTATION UPDATE)
PROFEIN UL21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
VIRIDAE: DS-DNA ENVELOPED VIRUSES; HERPESVIRIDAE; ALPHAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpes simplex virus (type 1 / strain hpem).
Ridae: ds-dna enveloped viruses; herpesviridae; alphaherpesvirikae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUDOMONAS AERUGINOSA.
ISUDOMONACIA GRACIIXCUTES; SCOTOBACTERIA; AEROBIC RODS AND
ISUDOMONADACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U8-08-951-733-20.rsp
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ID 01.21 HSV11
AC P10205;
DT 01-MAR-1989 (
DT 01-MAR-1989 (
DT 01-DEC-1992 (
DE PROTEIN UL21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREQUINCE FROM N.A.

A NABSIG S., HATTEMBRIST U., HOLLENBERG C.P., RAMERANI RAD M.;

A NABSIG S., HATTEMBRIST U., HOLLENBERG C.P., RAMERANI RAD M.;

LESTHITTER (CUTU-1955) TO ERBL/CERBANK, DOBJ DATA BANKS.

- C. - PATOMOSPHARE J. - CAUDYMNT-TRIN (CUT) - TANA (GLJ) = AMP +

C. - PATOMOSPHARE J. - CAUDYMNT-TRIN (CUT) - TANA (GLJ) = AMP +

C. - PATOMOSPHARE J. - CAUDYMNT-TRIN CUT AND J. - CAUDYMNT-TRIN STWIMENSE FAMILY.

C. - STREELLIFAR BEADORS TO CLASS I MAINOAUTI-TRIN STWIMENSE FAMILY.

C. - STREELLIFAR BEADORS TO CLASS I FALSE NEW J. - CAUDYMNT-TRIN STWIMENSE FAMILY.

C. - CAUDYMNT-TRIN STWIMENSE; PROTEIN BLOSTYPHENSE; LICASE; ATP-BINDING;

RM HITOCHOLEGE STREEL S. - CAUDYMNT-TRIN CUT AND J. - CAUDYMNT-TRIN STREEL S. - CAUDYMNT-TRIN STWIMENSE; ATP-BINDING;

RM HITOCHOLEGE S. - CAUDYMNT-TRIN CUT AND J. - CAUDYMNT-TRIN STREEL S. - CAUDYMNT-TRIN STWIMENSE; ATP-BINDING;

RM HITOCHOLEGE S. - CAUDYMNT-TRIN STWIMENSE;

RM HITOCHOLEGE 
      Search completed: Fri Dec 18 19:01:10 1998 Job time : 145 secs.
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Qy 1112 VPLLGSL 1118
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                                                                                                                                                                                                                                                                                                                                                  Query Match 0.68; Score 7; DB 1; Length 536;
Best Local Similarity 100.01; Pred. No. 5. 98e+00;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 5.98+60; Indels
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         59 LGSLRTA 65
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1115 LGSLRTA 1121
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P48525; 008201;
01-FED-1996 (REL. 3), CREATED)
01-WOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-WOY-1997 (REL. 35, LAST ANNOTATION UPDATE)
CLITAMT:-FRN STRIEFASS, MITOCHOMBRIAL (EC. 6.1.1.17) (CLITAMATE-TRNA
LICASE) (CLITMS).

WEEL ON TOLING STATEMENT AND STATEMENT STRIAN
ENCHAPHORICES CEREVISIAE (BAREN'S FEAST).
ENARTOR'S UPDATE AND STRIAN HEMILASCONICETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUCIANT H.

BULL INST. CHEM. RES., KYOYO UNIV. 71:338-342(1993).

BULL INST. CHEM. RES., KYOYO UNIV. 71:338-342(1993).

1 CARLITIC ACTIVITY RECOGNIZES THE DOUBLE-STRANDED SEQUENCES ACCO AND COGYO AND CLAMES RESPECTIVELY 10 BASES AFTER G-1.

AND 10 BASES REFORE G-1.

EMBL. D1788: 193131;

EMBL. D1788: 193131;

FIRECALSE. ROPOUTLEASE; NCCLEASE; RESTRICTION SYSTEM.

SEQUENCE 488 AA; 56737 NM; 2D74648E CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T201_MAGA STANDARD; PRT; 488 AA.
P43418;
01-MOV-1995 (REL. 32, CREATED)
01-MOV-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-WOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-WOV-1995 (REL. 32, LAST ANDOTATION UPDATE)
01-WOV-1995 (REL. 32, LAST ANDOTATION UPDATE)
1TPP III RESTRICTION ENERGY SCAI (SC 3.1.21.4) (EMONUCLEASE RGAI)
(R. 16411);
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717 LRVRAQD 723
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553 AAEHRLR 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRAIN-D273-10B;
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THITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENOPHÍLIUS CALLINARUM.
ORANOPHILUS (BRICILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
STEURELLACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1998
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(REL. 10, LAST SEQUENCE UPDATE)
(REL. 24, LAST ANNOTATION UPDATE)
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NEW MEDLINE: 97431088 AMEZIESON M., COUNTER C.K., EATON E.N., EL AN AMEZIESON M., COUNTER C.K., WELHERGE R.A.; BL EEL 90.185.39(1.99). BOR ELL 90.185.39(1.99).	REDURES 1700051 RE REDURES 1700051 RE RETURES 1700051 RE RETURES 1700051 RE RETURES 1700051 RE RETURES 271 RETURES 180.00 CORT TR.; RETURES 271 RETURES 271 RETURES 270.00 CORT TR.; RETURES 270.00 CORT	7-0 11 00:10:10 1000
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Page 26

Query Match 1.9%; Best Local Similarity 100.0%; Matches 22; Conservative

Score 22; DB 11; Length 67; Pred. No. 3.99e-42; 0; Mismatches 0; Indels 0;

Gaps

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SEMENTEED (CCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. AF029235; G2665903; -.
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5500ENCE 67 AA: 8368 NW; E2A06F2B CRC12;

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683 LESULWEBARREGLICASUGLIDDIBAWRFFULWERAQDEPELIFYKUDYTGANDT 742 601 LSELETWOHREARPALLTSRLEFTPKPDGLRFTVRDDYVGARTFBREKANERLTSRVFA 613 LSELETWOHREARPALLTSRLEFTPKPDGLRFTVRDDYVGARTFBREKANERLTSRVFA 623 LSELETWOHREARPALLTSRLEFTPKPDGLRFTVRDDYVGARTFBREKANERLTSRVFA 982 960

RESULT:

1 PRELIMINARY: PRT: 1122 AA.
1 070372; PRELIMINARY: PRT: 1122 AA.
2 070372; PRELIMINARY: PRT: 1122 AA.
2 070372; PRT: 1028 (PREMILEE, 07, CREATED)
2 01-AUG-1998 (PREMILEE, 07, LAST ANNOTATION UPDATE)
2 01-AUG-1998 (PREMILEE, 07, LAST ANNOTATION UPDATE)
2 02 02-1998 (PREMILEE, 07, LAST ANNOTATION UPDATE)
3 03 02-1998 (PREMILEE, 07, LAST ANNOTATION UPDATE)
4 02-1998 (PREMILEE, 07, LAST ANNOTATION UPDATE)
5 03 02-1998 (PREMILEE, 07, CRIN L., MORIN G.B., DEPINHO R.A.;
5 04 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 04 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP R.C., CRIN L., MORIN G.B., DEPINHO R.A.;
5 05 02-1998 (PR.A., ALAGOPP

Query Match 199; Score 22; DB 11; Length 1122; Best Local Similarity 100,0%; Prad, No. 199-42; Matches 22; Conservative 0; Hismatches 0; Indels

Indels 0;

Gaps 0

SEQUENCE FROM N.A. ALLSOPP R.C., CHIN L., MORIN G.B., DEPINHO R.A.; ONCOGENE 0:0-0(1998).

BMBL; AFOSIBLI: G3005592; E.
RNA-DIRECTED DAN POLYMERAS: .
SEQUENCE 1122 AA; 127977 NH; 22207506 CRC32;

RRW CEEMING CO. 035432 PRELIMINARY PRT: 67 AA.
035432 PRELIMINARY PRT: 67 AA.
035432 PREMICHEL 05, CREATED)
01-JAN-1998 (TREMBLERI. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLERI. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLERI. 07, LAST SHOOTATION UPDATE)
01-JAN-1998 (TREMBLERI. 07, LAST SHOOTATION UPDATE)
01-JAN-1998 (TREMBLERI. 07, LAST SHOOTATION UPDATE)
01-JAN-1998 (TREMBLERI.)
01-JAN-1998 (MOSE)
0 SEQUENCE FROM N.A.
DRISSI R., CLEVELAND J.L.;

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Dec 21 09:28:30 1998
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ENQUENCE FROM N.A.
MEDLING, 8908663.
SACA Y. TUNG J.S., SHEN F.W., PANCOAST T.C., BOYSE E.A.;
FACA Y. TUNG J.S., SHEN F.W. W., PANCOAST T.C., BOYSE E.A.;
MCL. SILL, 84.089-4895(1989).
BEBL: MAJ3154 C.5543317VB SPLICING; TRANSMEMBRANE.
MAJERNA J. A. A. A. ZIII MN; 7A10DDDA CRC31;
SEQUENCE 24 AA; 2717 MN; 7A10DDDA CRC31;

Query Match 0.8%; Best Local Similarity 100.0%; Matches 9; Conservative Score 9; DB 11; Length 24; pred. No. 9.84e-04; 0; Mismatches 0; Indels 0 Gaps

8 B Omery Match 0.8%; Score 9; DB 11; Length 183; Best Local Similarity 100.0%; Pred. No. 9:84e-04; Matches 9; Conservative 0; Mismatches 0; Indels 8 LAFGFALLD 16 |||||||| 119 LAFGFALLD 127 . Caps

0

US-08-951-733-20.rspt

10 LAFGFALLD 18 |||||||| 119 LAFGFALLD 127

RESULT 6

10 1814 PRELIMINAT: PRT: 183 AA.

AC 61814 PRELIMINAT: D. LAST SEQUENCE UPDATE;
DT 01.WV-1986 (PREMBLED: 0.) LAST SEQUENCE UPDATE;
DT 01.WV-1986 (PREMBLED: 0.) LAST MANOTATION UPDATE;
DE LY-5 GLYCOPECTEM PREMBLED: 0.) LAST MANOTATION UPDATE;
DE MUS MISCOLUS (NODER)
CC EXTRACTION (ACTACON) CHONEDATA: VERTEBRATA: TETRAPODA: MAMALIA:
RM 111
RP SEQUENCE PROM N.A.

RM MEDLINE: R7260987:
RM MEDLINE: R7260987.
RM SAGAT. TUNG J.S. SHEN F.M., BOYSE F.A.:
PROC. NATL. ACAD. SCT. U.S.A. 84:5364-5368(1987).
DR EMBL: M1730: GG21198: PROC. NATL. ACAD. SCT. U.S.A. 84:5364-5368(1987).
RW SIGNAL ALTERNATIVE SPLICING.
PT SIGNAL ALTERNATIVE SPLICING.
PT SIGNAL ALTERNATIVE SPLICING.
PT NOW_TER 183 LY-5 GLYCOPROTEIN.

FT NOW_TER 183 LY-5 GLYCOPROTEIN.

SEDURNCE PROM N.A.
SEDURNCE PROM N.A.
SEDURNCE 197360987.
SAGA T. TURG J.S. SHEN F.M., BOTGE E.A.;
SPACE LATTL ACAD. SCI. U.S.A. 84:5364-5368(1987).
PROC. BATIL ACAD. SCI. U.S.A. 84:5364-5368(1987).
SEGURL ALTERNATIVE SPLICING
SEGURL ALTERNATIVE SPLICING
SEGURL ALTERNATIVE SPLICING
SEGURL ALTERNATIVE SPLICING
SEGURAL ALTERNATIVE SPLI

EUKARYOTA; METAZOA; CHORDATA; EUTHERIA; RODENTIA.

STERRERRS

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Page 27

TRESULT 5
PRELIMINARY; PRT; 24 AA.

1D 061815
PRELIMINARY; PRT; 24 AA.

1D 01815;
PRT 01 NOV-1996 (TREMBLEEL 01, CREATED)
PR 10 NOV-1996 (TREMBLEEL 01, LAST REQUENCE UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST REQUENCE UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST RANOTATION UPDATE)
PR 10 NOV-1996 (TREMBLEEL 01, LAST RANOTATION UPDATE)
PR 10 NOVE 1996 (TREMBLEEL 01, LAST RANOTATION UPDATE)

MUS MUSCULUS (MOUSE).

US-08-951-733-20.rspt

Page 28

Ouery Match 0.8%; Score 9; DB 4; Length 632; Best Local Similarity 100.0%; Pred. No. 984e-04; Matches 9; Conservative 0; Mismatches 0; Indels 0 Caps

515 VRAQDPPPE 523 |||||||| 719 VRAQDPPPE 727

RESULT

1D 0.1319;

AC 0.1319;

DT 0.1.3M.*1998 (TREMBLEEL. 05, CREATED)

DT 0.1.3M.*1998 (TREMBLEEL. 05, LAST SEQUENCE UPDATE)

DT 0.1.3M.*1998 (TREMBLEEL. 05, LAST SEQUENCE UPDATE)

DT 0.1.3M.*1998 (TREMBLEEL. 07, LAST SHOCKATION UPDATE)

DT 0.1.3M.*1998 (TREMBLEEL. 07, LAST SHOCKATION UPDATE)

DE TELOMERASE REFERSE TRANSCRIPTASE 1.

GN TRIL.

OS TELOMERASE REFERSE TRANSCRIPTASE 1.

GN TRIL.

OS TELOMERASE REFERSE TRANSCRIPTASE 1.

RE SUDJUNCE PROM N.A.

RE STRAIN=972H:

RA LINGUEN J. HARLEY C.B., CEMPHAN K.B., WEINRICH S.L.,

RA LINGUEN Z. HARLEY C.B., CEMPHAN K.B., WEINRICH S.L.,

RA LINGUEN Z. HARLEY C.B., CEMPHAN K.B., WEINRICH S.L.,

RE SEQUENCE Z719:955-955(1997).

RN [2]

RN SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

ALYES M., NAANDERAM N.A., BARRELL B.G., VOLCMARRI G.;

SEQUENCE PROM N.A.

STRAIN-972H:
MEDLINE: 9400623

MEDLINE: 9400623

MEDLINE: 9400621

MEDLINE: 97100621

SENOUENCE FROM N.A. STRAIN-972H-LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.;

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RESULT 9

ID 01338;

PRELIMINARY: PRT: 999 AA.

AC 01338;

DT 01.3N.1998 (TREMELEL. 05, CREATED)

DT 01.3N.1998 (TREMELEL. 05, LAST SEQUENCE UPDATE)

DT 01.3N.1998 (TREMELEL. 05, LAST SEQUENCE UPDATE)

DT 01.3N.1998 (TREMELEL. 05, LAST SEQUENCE UPDATE)

DT TLIMERASE REMESSE TRANSCRIPTASE 1.

RETLIMERASE REMESSE TRANSCRIPTASE 1.

STRILES PROM MA.

RE STRAINS PROM MA.

RE STRAINS PROM MA.

RE STRAINS T.M., DREIN G.B., CHAPMAN K.B., WEINRICH S.L.,

RA KLINGER J., HALLE C.B., CECH T.R.;

RA KLINGER 277. 952-95(1997)

DR EMEL PROMISSION FOLIMERASE.

SE SEQUENCE 989 AM. 116456 MM; PDE74202 CRC32:
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TRESULT 12

ID 065210; PRELIMINARY; PRT; 146 AA.

AC 065210; 05210; CREMBUREL. 01, CREATED;

DT 01-NOV-1996 (TREMBUREL. 01, LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.89; Score 9; DB 3; Langth 988; Best Local Similarity 100.0%; Pred. No. 9.84e-04; Endels Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.8%; Score 9; DB 3; Length 989;
Best Local Similarity 100 0%; Pred. No. 9.84e-04;
Matches 9; Conservative 0; Mismatches 0; Indels
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O61812 PRELIMINARY: PRT; :
O61812;
O1-NOV-1996 (TREMBLREL: O1, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1343 1343
SEQUENCE 1343 AA; 150679 MW; 984DFAEB CRC32;
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NAKANDAN TM., MORIN G.B., CHAPMAN K.B., WEIRRICH S.L., ANDREWS H.B., LIKHGER J., HARLET C.B., CECH T.R., SCIENCE 27.955-595(195).

ENGL: APOLS783, G2340165; ...
FRAL: PRODIST83; rt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA E EMBL; AF015783; C2340168 - .
EMBL: AF015783; E1285580 - .
FRAM: PP00078; FTC.
RNA-DIRECTED DANA POLYMERASE.
SEQUENCE 988 AA; 116328 NH; 39C185A7 CRC12;
                                                                                                                                                                                                                                       8 LAFGFALLD 16
{|||||||
119 LAFGFALLD 127
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|||||||||
852 GIPQGSILS 860
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|||||||||
852 GIPQGSILS 860
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                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 11; Length 1343;
Pred. No. 9.84e-04;
0; Hismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1291
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DO 064730;

PRELIMINARY: PRT; 1343 AA.

AC 064730;

PT 01-807-1996 (TREMEREL 01, CREATED)

PT 01-807-1996 (TREMEREL 01, LAST SEQUENCE UPDATE)

PT 01-807-1996 (TREMEREL 01, LAST SEQUENCE UPDATE)

PT 01-807-1996 (TREMEREL 01, LAST ANDOMITON UPDATE)

DE LEUCCOTTE COMMON ANTIGNN (L-CA) (FRAGMENT).

ON EUTHANTOTA, METAKOA, CHORDATA; VERTERRATA, TETRAPODA, MAMMALIA;

RE 11

RE 12

RE 12

RE 12

RE 12

RE 12

RE 12

RE 13

RE 14

RE 14

RE 15

RE 14

RE 15

RE 16

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Best Local Similarity 100.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECURNCE FROM N. A. RASCHER W.C.;
RENDEZE S.L., BARRITT D.S., RASCHER W.C.;
RENDL HOUSE, 1443-254(1991).
RENDL HOUSE, GLOSSIT.
ROD; NOT:97810; PTPRC.
PROSITE: PS00383; TET. PROSPHATASE.1; 2.
PFMA: PF00041; f.d.
PFMA: PF00041; T.D.
PFMA: PF00041; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BA71V;
MEDILINE; 9113498.
CAMACHO A., VINUELA E.;
VINOLOGY 181: 251-257(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL 1 23 POTENTIAL.
CHAIN 24 1291 LYMPHOCTIE COMMON ANTIGEN.
SEQUENCE 1291 MA; 144559 MY; 63481A8D CRC32;
SEQUENCE FROM N.A.
STRAIN=BA71V;
MEDLINE; 93346971.
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PDP146L.
DP146L.
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01-UNN-1998 (TREMELEEL, 05, LAST RECEPTOR TYPE, C PRECUNSOR (EC 3.1.3.48)
PROTEIN TROCKINE PROSPHANASE, RECEPTOR TYPE, C PRECUNSOR (EC 3.1.3.48)
PEPROC OR LYS.
PEPRO OR LYS.
HIS MOSCULUS (MOUSE)
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HIS MOSCULUS (MOUSE)
EXPLANOTA, METALOA, CHORDATA; VERTEBRATA; TETRAPODA; MANGALIA;
EXPLANOTA, MOTERIA.
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STRALIN-ANY.
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A VERA I. BLASCO R. YINUELA E.;
A VERA I. BLASCO R. YINUELA E.;
A VERA I. G4:2073-2081(1990).
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STRAINEATIV:
TANEE R.J., RODRIGUEZ J.M., P
RODRIGUEZ J.P., VINUELA E.;
TANEOLOGY 208:249-278(1995).
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119 LAPGFALLD 127
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STRAIN-BA71V;
LA VEGA I., GONZALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEQUENCE FROM N.A.
STRAINSBATIV;
SEDILNE; 90219204.
LIMENDRAL J.M., ALMAZAN F., 1
LVIROL. 64:2064-2072(1990)
                                                                                                                                   EQUENCE FROM N.A.
TRAIN-BAZZE

EDILME: 94187118.

EDILME: 94187118.

EDILME: 7 ANEZ R.J., PAN R.,

NUELA E.,

VIROL. 68:2746-2751(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                               RAIN-BA71V;
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RIDAE: DS-DNA NONENVELOPED VIRUSES;
                                                                                                                                                                                                                                                                                                                                                                          GEN. VIROL. 0:0-0(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEGA I., GONZALEZ A., BLASCO R.,
ROLOGY 201:152-156(1994).
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Pred. No. 9.84e-04;
0; Mismatches 0; Indels
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                                                                                                                                                                                                             RODRIGUEZ J.F.,
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Best Local Similarity 100.0%;
Matches 8; Conservative
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STRAIN-BA71V;
MEDLINE; 92087485.
RODRIGUEZ J.M. SALAS M.L., V
VIROLOGY 186:40-52(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR-BATIV;
MEDLINE; 9408574.
YANEE R.J., RODRIGGEZ J.M., E
GENE 134:161-174(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 RSYLPNTV 14
||||||||
142 RSYLPNTV 149
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    SENDURNEE FROM N.A.
STRAIN-COOPER,
KIADA N., TIKOO S.K., BABIUK L.A., HURK S.;
GENE G.0-0(0).
ESBUL: U3493; G114326; ...
ESBUL: U3493; G114326; ...
ESBUL: U3493; G114326; ...
ESBUL: U3493; G114326; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XNREK R.J.;
SUBALTITED (DEC-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL. D18466; G780518; .
SEQUENCE 146 AA; 17258 NN; 82574504 CRC32;
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STRAIN=BA71V:
MEDLINE: 944123986.
RODRIGUEZ J.M., YANEZ R.J.,
GENE 138:103-110(1993).
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STRAIN-BAIV,
RODRIGUEZ JA. YANEE R.J., ALMEAN F.,
J. VIROL. 67:5312-5320(1993).
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J., GEN. VIROL. 74:1633-1638(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEROLENCE PROM N.A.
STRAIN-RANJU;
REDILIE: 8016328
GONEALEZ A., TALAYERA A., ALMENDRAL J.M., VINUELA E.;
NUCLEIC ACIDS RES. 14:6835-6844(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMOLEME PROM N.A.
SEMOLEME POOM N.A.
SEMOLEME SOLIGOS
RODRIGUEZ F. ALCARAZ C., EIRAS A., YANEZ R.J.,
ALONSO C., RODRIGUEZ J.F., ESCHIMANO J.M.;
J., YIMOL. 68:7344-7255(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŠEOŪENCE FROM N.A.
STRAIM=BATIV;
STRAIM=BATIV;
MEDLINE; 90223993.
LOPEZ-OTIN C., FREIJE J.M., PARRA
LOPEZ-OTIN C., FREIJE J.M., PARRA
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STRAIN-BATYL
STRAIN-BATYL
STRAIN-BATYL
STROID N., PERLEY J.M., SALAS N.L., VINUELA E., LOPEZ-OTIN C.;
ARCH. VIROL. 130:93-107(1993).
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STRAINEMATYS
REDILTES, 93281390.
TANEE R.J.: BOOGSTELL M., NOCAL M.L., TUSTE L., VINUELA E.;
PUCLEIC ACIDS RES. 31:3433-3437(1993).
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STRAIN-BA71V;
MEDLINE; 90357780.
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STRAIN-BA71V;
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TRAIN-BA71V;
ANEZ R.J.;
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LCAMI A., ANGULO A., VINUELA E.;
...GEN. VIROL. 74:2317-2324(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDLINE; 90357780.
ASCO R., LOPEZ-OTIN C., MUNOZ M., BOCKAMP E.O., SIMON-MATEO C.,
KNUELA E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09:28:30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 8; DB 14; Length 146;
Pred. No. 1.57e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VINUELA
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                                                                                                                                                                                                                HERPESVIRIDAE; ALPHAHERPESVIRINAE
                                                                                                                                                                                                                                                                                                                                                                                                                  338 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VINUELA E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT. 14

ID 083745; PRELIMINARY, PRT; 342 AA.
AC 083745; PREDELREL 01, CREATED)
DT 01-NOV-1996 (TREMELREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMELREL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMELREL 01, LAST SEQUENCE UPDATE)
DT PROVIENT, V-90S.
OS MYZLOPOLIFERANTITE SARCOMA VIRUS.
OC VIRILAR, SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
RN 110-TREME 40216451.
RN MEDILIE; 40216451.
RN STRUERCE TA. AAMSTEROTT C. ROLLEK R., COOGINS L., OSTERTAG W.;
RN STRUERCE A. ARSTEROTT C. ROLLEK R., COOGINS L., OSTERTAG W.;
RN STRUER A. (ABSTEROTT C.)
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RESULT 15
ID 011254, PRELIMINARY; PRT; 500 AA.

C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254, C 101254
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Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local Similarity 100.0%;
Matches 8; Conservative
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SEQUENCE FROM N.A.
STRAITS STRAITS AT STRAITS STRAITS STRAITS STRAITS STRAITS STRAITS C., PREIJE J.M., ANDRES G.
VIROGET 206:1140-1144(1995).
                                                                                                                                                                                                                                                                                                                                                                                       291 LRPSLTGA 298
||||||||
372 LRPSLTGA 379
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||||||||
| 243 ARRRGGSA 250
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STRAIN-BA71Y;
MEDLINE; 92263907.
GARCIA-BENTO R., FREIJE J.M., LOPEZ.
SALAS M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŚEQÓZNCE FROM N.A.
STRAINBATIV;
KEDLINE; 93174941.
PENA L., TANEZ R.J., REVILLA Y.,
PUROLOGY 193:319-328(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-BA71V;
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STRAIN=8,711V;
NEDLINE; 933310.
PRADOS F.J., VINUELA E., ALCAMI
PRADOS F.J., VINUELA E., ALCAMI
J. VIROL. 67:2475-2485(1993).
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STRAIM-BATIV;
HEDLINE; 94091056.
PRETIE J.M., LAIN 9., VINUELA E.,
VINUS RES. 30:63-72(1993).
[25]
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STRAIN-BA71Y,
REDLINE; 92260660 A, LOPES-OTIN C.,
ALCANI A, ANGULO A, LOPES-OTIN C.,
ALRANGOGA AL, VINDELA E.;
7 VIROL. 66:3860-3868(1997).
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IMON-MATEO C., ANDRES G., VINUELA E.;
MBO J. 12:2977-2987(1993).
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ANEZ R.J., VINUELA E.;
IROLOGY 193:531-536(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ROLOGY 188:938-947(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8: DB 14: Length 342:
Pred. No. 1.57e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8; DB 14; Length 338;
Pred. No. 1.57e-01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VINUELA E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lopes-Otin
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D72174 PRELIMINARY PRT; 23 AA.
C 027174;
C 027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 100.0%;

Matches 8; Conservative
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C TISSUE-ADRESMA, CLAMD;

X HEDLINE; 97208876.

A ROWERA C., MANDAYASSII C., NISHIMORI K., MIZUNO S.;

L GENE 185:217-222(1997).

C 1- SINILARIT: BELOWS TO THE CITOCHROME P450 FAMILY.

R EMBL. P450036: CITOCHROME_P450; 1.

R PROSITE: P500085: P55000XGENASE. ELECTROM TRANSPORT; HEMBANNE; HEMBANNE TRANSPORT; HEMBANNE; HEMBANNE SOURCE SOB AA: 58195 NY: 88384C4F CRC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.7%;
Best Local Similarity 100.0%;
Matches 8; Conservative
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||||||||
426 PYGVLLKT 433
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060300 PRELIMINARY; PRT; 1095 AA.
060300 PREMIMENT; PRT; 1095 AA.
060300 PREMIMENT; O7, CREATED)
01.AGC-1988 (TREMIMENT, O7, LAST SEQUENCE UPDATE)
01.AGC-1988 (TREMIMENT, O7, LAST ANNOTATION UPDATE)
01.AGC-1988 (TREMIMENT);
01.AGC-1988 (TR
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||||||||
953 CGLLLDTR 960
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||||||||
15 ALAPATPA 22
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||||||||
559 REEILAKF 566
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BURLANTOTA, PROPOZOAN, SARCOMASTIGOPHORA, SARCODINA, RHIZOPODA;
BUNYCETOZOA, DICTYOSTELIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
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HARAN O.,
NA RES. 5:31-39(1998),
REB.; ABO11125; D1026409; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W.F., IRANFAR N.;
TED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA
AF019982; G2425115; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 8: DB 4: Length 1095;
Pred. No. 1.57e-01;
0: Mismatches 0: Indels
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Pred. No. 1.57e-01;
0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-951-733-20.rspt
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DO 05812: PRELIMINARY: PRT: 37 AA.
AC 05812: PREDILECT. 07, CREATED)
DT 01.ACC.1988 (PREDILECT. 07, CREATED)
DT 01.ACC.1988 (PREDILECT. 07, LAST SEQUENCE UPDATE)
DT 01.ACC.1988 (PREDILECT. 07, LAST SEQUENCE UPDATE)
DT 01.ACC.1988 (PREDILECT. 07, LAST SEQUENCE UPDATE)
DE LICOCRESION SEQUENCE (PRACHETIN UPDATE)
DE LICOCRESION SEQUENCE (PRACHETIN, ANGIOSPERMAE: DICOTILEDONEAE:
CULNARYOR, PLANTN: EMBROPHITA, ANGIOSPERMAE: DICOTILEDONEAE:
RE SUBLINCY, ALISA, CRASS.
RE SERALHCY, ALISA, CRASS.
RE SERALLCY, ALICA, ALICA, CRASS.
RE SERALLCY, ALICA, CRASS.
RE SERALLCY, ALICA, CRASS.
RE SERALLCY, AL
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DO GA144

AC GA144

DT G
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AC 024505; PREMICEL 05, LA
DT 01-JVN-1990 (TREMELEZ. 05, LA
DT 01-JVN-1990 (TREMELEZ. 06, LA
DT 01-JVN-1990 (TREMELEZ. 06, LA
DT 01-JVN-1990 (TREMELEZ. 06, LA
DE CENAMON (PALEY); PRANTA EMBRIOPHTIA
RN (1978-LES) GAMANRAE.
RN 1251002 FROM 1978-1978
RN 1251002 FROM 197
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 6; Conservative
                                                       Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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STRAINSTOT.

MEDILIE: 9535569

BECENT P. STINAD P. S. MCCARTY D.R.;

SCIENTE 77::406-4409(1996)

BEDL: UT-422 G1597731

PROSITE: BEGOLOG: TERR.G.

PRAM: PFO0050: TERR.G.

PRAM: PFO0050: PROSITE CRIMITY.

SEQUENCE 901 AN: 97438 MW; 90597240 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 VSTLTDL 13
|||||||
785 VSTLTDL 791
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STRAINFOA-2)
MEDILIER, 96059477.
MADEDDU L. GANTIER H.C., VAYSSIE L., HOUARI A., SPERLING L.;
MADEDU L. CELL 6:69-659(1995).
EMBL; U77510, 6881410; -.
MARHEN PROTEIR.
10M.TER 12
10M.TER 23
1
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EURANYON, PLANYA, EMBRYOPHYTA; ANGIOSPERMAE; NONOCOTTLEDONEAE:
CYPERALES; GRAMINEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 SRSLPLPK 437
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|251 SRSLPLPK 258
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NON_TER 37 37
SEQUENCE 37 AA; 4205 MW;
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STRAIN-D4-2;
MEDILIS: 93119139.
MADEDUD L., GAUTIER M.C., LE CAER J.P.,
BACKHINIE 76:329-335(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8; DB 5; Length 869;
Pred. No. 1.57e-01;
0; Mismatches 0; Indels
                                                       Score 7; DB 10; Length 37; Pred, No. 1.47e+01; 0; Mismatches 0; Indels
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Pred. No. 1.47e+01;
0; Mismatches 0; Indels
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RESULT 26

OR OSCIONAL PRELIMINARY: PRT: 117 AA.

TO COSCIONAL PRELIMINARY: PRT: 117 AA.

TO COSCIONAL PRELIMINARY: PRT: 117 AA.

TO COSCIONAL PROPERTY OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 23
ID 03380
PRELIMINARY; PRT; 109 AA.
AC 03380;
DT 01.NOV-1996 (FREMELREL 01. CREATED)
DT 01.NOV-1996 (FREMELREL 01. LAST SEQUENCE UDDATE)
DT 01.NOV-1996 (FREMELREL 01. LAST SEQUENCE UDDATE)
DE HEPA (FRAMEMET)
DE HEPA (FRAMEMET)
OS STREPPOCOCCIG CRISTA.
OG PLASHID POCRAOO2.
OC PROKARYOTA; BACTERIA; FIRMICUTES; GRAM-POSITIVE COCCI;
OC STREPPOCOCCICCALE.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-CCAA;
DATERIA F.F., DIRIENZO J.M., NCRAY T.L., ROSAN B.;
RH (1)
REC STRAIN-CCAA;
DR HERLY (1)
RN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REAL STREET, S
                     RESULT 27
ID 073311
AC 073311;
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C STRAINH2 4 1.23
X MEDILINE: 9065223.
X MEDILINE: 9065223.
X MEDILINE: 9065223.
X MEDILINE: 9065223.
X MEDILINE: 906523.
X MEDILINE: 9065223.
X MEDILINE: 906522.
X
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%; Pred No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                         65 ARRRGGS 71
|||||||
243 ARRRGGS 249
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152 ALRGSGA 158
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|||||||
183 LVAPSCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLASHID.
SEQUENCE 87 AA: 9613 MW; 3DE25EOA CRC32;
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052175 PRELIMINARY: PRT: 87 A.
01-7UN-1998 (TREMBLEEL. 06, CREATED)
01-7UN-1998 (TREMBLEEL. 07, LAST SEQUENCE UPDATE)
01-7UN-1998 (TREMBLEEL. 07, LAST SEQUENCE.
01-7UN-1998 (TREMBLEEL. 07, LAST SEQUENCE.
01-7UN-1998 (TREMBLEEL. 08, LAST SEQUENCE.
01-7UN-1998 (TREMBLEEL. 09, LAST SEQUENCE. 09, LAST SEQUENCE.
01-7UN-1998 (TREMBLEEL. 09, L
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|||||||
364 RPSFLLS 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

HANES D.E., KEASLER S.P., LAMPEL K.A.;

SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS

SUBMITTED (SEP)

GEBL, PF025795; G2689636; ...
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ROBISON K.;
ROBISON K.;
SEDEMITIED (SEP-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; U15181; G899267; ...
SEQUENCE 117 AA; 12770 NH; BEAZ4CE6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7; DB 2; Length 117;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; DB 2; Length 87;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels 0;
                                                                                      PRT;
                                                                                      125
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RESULT 28

ID 05591:
D 05591:
D 05591:
DT 01-NOV-1996 (TRENDELEEL. 01. CREATED)
DT 01-NOV-1996 (TRENDELEEL. 01. LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TRENDELEEL. 01. LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TRENDELEEL. 01. LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 14.4 KD PROTEIN.
OS SYNECHCUSTIS SP.
OC CHROCOCCALES.
OC CHROCOCCALES.
RN [1]
RN 1510
RN 1520
RN 1540
RN 1
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IREGOLATED PRELIMINARY: PRT: 111 AA.
AC Q04233 PRELIMINARY: PRT: 111 AA.
AC Q04233 PRELIMINARY: PRT: 111 AA.
AC Q04233 PRELIMINARY: PRT: 111 AA.
CQ04233 PRELIMINARY: O1. LAST REFORMED UPDATE)
DT 01-FED-1997 (FREDELEEL. 02.) LAST ANSOCATION UPDATE)
DE HYPOTHETICAL 12.3 ND PROTEIN.
OS HANSENULA POLYMORPHA (TEAST).
CENTANTOTA: FUNCI ASCONYCOTINA: HEMIASCONYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRALFEDLIA A.I. SEREDINA S.A. TIKHONINOVA L.P., KRTUK
DE MENTICAL PROTEIN.
THE PROTEITICAL PROTEIN.
SQ SEQUENCE 111 AA. 12291 NN; 39D4883A CRC32;
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ID 053100 PRELIMINART; PRT: 113 M.

ID 053100 PRELIMINART; PRT: 113 M.

ID 053100 PRELIMINART; PRT: 113 M.

ID 053100 PRT: 1996 (TREMBLERE, 01, CREATED)

ID 1. NOV-1996 (TREMBLERE, 01, LAST SEQUENCE UPDATE)

ID 1. NOV-1996 (TREMBLERE, 01, LAST SEQUENCE UPDATE)

ID 04F37 PRACHETY;

ID 05F37 PRT: 113 M.

ID 05F37 PRT: 113
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[||||||
Qy 699 GASVLGL 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FT NON_TER 1 1 1 SQ SEQUENCE 109 AA; 11728 MW; DODP954B CRC32;
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.6%; Score 7; DB 2; Length 109; Best Local Similarity 100.0%; Pred. No. 147e+01; Matches 7; Conservative 0; Mismatches 0; Indels 0;
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|||||||
330 PSTSRPP 336
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STRAIN-DLI,
STRAIN-DLI,
STRAIN-DLI,
STRAIN-DLI,
STRAIN-DLI,
SERVILLEN, A.I., SERDIRN, S.A., TIKBONIROVA L.P., KRYUKOV V.M.;
SUNMITTED (APR. 1991) TO EMBL/GENBANK/DDBJ DATA BARKS.
DBLI, X58862, G2764.
SECURENICAL PROTEIN
SECURENICAL PROTEIN
SECURENICAL PROTEIN
SECURENICAL PROTEIN
SECURENICAL PROTEIN
SECURENCE 111 AA; 12291 MM; 39D4883A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 TSRLRFI 28
|||||||
640 TSRLRFI 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOURTER 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRASŠLY N., XIANG S., ARIYOSHI K., AABY P., JENSEN H., DIAS P., WHITTLE H., BRUUER J.; SERUER J.; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE OPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
04. PROTEIN (FRACHENT).
          STRAIN-POCESSI;
STRAIN-POCESSI;
KANERO T. TARATA S., SATO S., KOTANI H., SAZUKA T., KIYAJIKA N.,
SGUZURA M., TARATA S., SEGUIRA M., SEGUIRA M., TARATA S., SEGUIRA M., SEGUIRA M., TARATA S., SEGUIRA M., SEGUIRA M., SEGUIRA M., SEGUIRA M., SEGUIRA M., SEGUIRA M., SEGUIRA S., SEGUIRA M., SEGUIRA M., SEGUIRA S., SEGUIRA M., SEGUIRA S., SEGUIRA M., SEGUIRA S., SEGUIRA S., SEGUIRA M., SEGUIRA M., SEGUIRA S., SEGUIRA M., SEGUIRA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRAIN-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IANG 2., ARIYOSHI K., WILKINS A., DIAS F., WHITTLE H., BREUER J.:
IDS RES. HUM. RETROVIRUSES 13:501-505(1997).
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INIDAE, SS-RHA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
ENTIVIRINAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125; 13505 MW; FC04002C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 3; Length 111;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7: DB 14: Length 125:
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OXYPHOTOBACTERIA; CYANOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-951-733-20.rapt
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    822
EMBL; D64005; G1006607; -.
HYPOTHETICAL PROTEIN.
SEQUENCE 128 AA; 14443 MW; 2C040B5B CRC32;
                                                                                       US-08-951-733-20.rapt
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B Ş Osery Match 0.6%, Score 7, DB 2; Length 128; Best Local Similarity 100.0%; Pred. Ro. 147e+01; Matches 7; Conservative 0; Mismatches 0; Indels 9 Caps 9

RESULT 29

PRELIMINARY: PRT; 135 A.

AC 000839

PRELIMINARY: PRELIMINARY: PRT; 135 A.

AC 01 TAX 2.

GR TAX 3.

GR TAX 3

Oery Match 0.6%; Score 7; DB 14; Length 135; Best Local Similarity 100.0%; Pred No. 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels 0; 72 SRSLPLP 78 ||||||| 251 SRSLPLP 257 Gaps

Ş 8

PRELIMINARY; 01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE) PRT; 138 ζ

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Mon
                                                                                                                          ID 98023 PRELIMINARY;
AC 980823 PRELIMINARY;
DT 01-WOY-1996 (TREMSLEEL. 0
DT 01-WOY-1996 (TREMSLEEL. 0
DT 01-WOY-1996 (TREMSLEEL. 0
DT 01-WOY-1996 (TREMSLEEL. 0
DT NOTEIN 22/20XIII.
9
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PRO PR (FRAGMENT).

REY. NO TOTAL LIMPHOTROPIC VIRUS TYPE II.

WINDLE: SS-RNA MOMENTALOPED VIRUSES; POSITIVE STRAND |

RETROVIRIDAE; ONCOVIRUSES.

RAMMALIAN TYPE C ONCOVIRUSES. 084408 PRELIMINARY PRT: 149 AA.
084408 PRELIMINARY PRT: 149 AA.
0814001
01-NOV-1996 (TREMELEEL. 01. CREATED)
01-NOV-1996 (TREMELEEL. 01. LAST SEGURACE UDDATE)
01-UN-1998 (TREMELEEL. 05. LAST ANNOTATION UDDATE)
T-CELL LYEMPHOPIC VIRUS TIPE 2 REX AND TAX GENES, PARTIAL CDS, CLONE
PCC PX (FRAGMENT). RXA

SECURNCE FROM N.A.
HEDLINE, 9610944.

HEDLINE, 9610944.

OLIVIERA H. D., OLIVIERA O.D., ISHAK R.,
OLIVIERA H. P., LARRENG D., ISHAK M., ACCYEDO V., HAMMERSHLAK N.,
ISHAK N.,
J. FUR. D., 1971-1971-1981.

J. FUR. D., 1971-1981.

DEBL., 1971-1981.

DEBL., 1971-1981.

OLIVIERO, 1971-1981.

NON_TER 1 1 1 SEQUENCE 149 AA; 15702 MW; 483CD5A5 CRC32;

문 overy Match 0.6%; Score 7; DB 14; Length 149; Best Local Similarity 100.0%; Pred. No. 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels 86 SRSLPLP 92 |||||||| 251 SRSLPLP 257 0 Caps 0

RESULT 33

RESULT 33

RESULT 34

RESULT 35

RESULT 36

RESULT 37

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877 R P P

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Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative EHU S.M., KUBO T., BALL W.M.; J. VERGL, 70:1483.114921996). EMGL; U2872; G1463038; -. NON_YER BOUERCE 149 AA; 15779 NW; 5E356C3B CRC32; Score 7; DB 14; Length 149; Pred. No. 1.47e+01; 0; Mismatches 0; Indels 0

86 SRSLPLP 92 ||||||| 251 SRSLPLP 257

HOMAN T-CELL LYMPHOTROPIC VIROS TYPE II. VIRIDAE; SS-RNA MORENVELOPED VIROSES: POSITIVE STRAND RNA VIROSES RETROVIRIDAE; GNOCVIRINAE; ETPE C ONCOVIRIDS GROUP; NAMALIAN TYPE C ONCOVIRIOSES.

PARTIAL CDS,

RESULT 34

IN CORRECT PRELIMINARY: PRT: 149 AA.
AC GR3377.

DT 01-NOV-1996 (TRENDLEEL. 01 CREATED)
DT 01-NOV-1996 (TRENDLEEL. 01 LAST RECORREC UPDATE)
DT 01-NOV-1996 (TRENDLEEL. 01 LAST RECORREC UPDATE)
DT 01-NOV-1996 (TRENDLEEL. 01 LAST AND TAX GENES, PART 1991 TRENDLEEL. 02 LAST AND TAX GENES, PART 1991 TRENDLEEL. 02 LAST AND TAX GENES, PART 1981 TRENDLEEL TRENDLEEL TRES 2 REX AND TAX GENES, PART 1982 TRENDLEEL AND TAX GENES, PART 1982 CONCOVIRUS GROUP;
CO RAMADALAN TYPE CONCOVIRUSES.
RN 111
RN 121 TRENDLEEL AND TAX GENES C. OLIVIERA M.D., OLIVIERA SENDIENCE FROM N.A.
SENDIENCE FROM N.A.
SENDIENCE, 96190544.
EZIDAKE 96190544.
EZIDAKE N. KOVAO P., MONKEN C., OLIVIERA N.D., OLIVIERA O.D., ISHAK R.,
DIUNZERA M.P., LAUGERRO P., ESHAK M., ACEVEDO V., HAMMERSHIAK N.,
EHU S.M., KUBO T., HALL M., SENAK M., ACEVEDO V., HAMMERSHIAK N.,
EHU S.M., KUBO T., HALL M., SENAK M., ACEVEDO V., HAMMERSHIAK N.,
EMBL_M., 123074; 14165044; 7.
EMBL_M., 123074; 14165044; 7.

Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative NON_TER 1 1 1 3 3 3 3 2 5 5 1 C RC 3 2; SEQUENCE 149 AA; 15748 MW; 3D 3 2 5 5 1 4. Score 7; DB 14; Length 149; Pred. No. 1.47e+01; 0; Mismatches 0; Indels 0 eda3 9

ŝ 86 SRSLPLP 92 ||||||| 251 SRSLPLP 257

RESULT 35 ID Q82405 PRELIMINARY; PRT; 149

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HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE II.
VIRIDAR; SS-RMA ROMENVELOPED VIRUSES; POSITIVE STRAND RNA VIRUSES;
RETROVIEIDAE; ROMCOVIENUSE; TYPE C ONCOVIRUS GROUP;
MANDALIAN TYPE C ONCOVIRUSES.

SEQUENCE FROM N. A.
MEDILINE 952916.
CIMINALE V. D'AGOSINO D.M., SOTTI L., FRANCHINI G.,
CHIZOLOC PLANCH L.,
EMBL. 144578 (1982),
EMBL. 144578 (198298),
SEQUENCE 138 AA; 14516 NF; EA0983AO CRC32; FELBER

Query Match 0.6%; Best Local Similarity 100.0%; Matches 7; Conservative Score 7; DB 14; Length 138; Pred. No. 1.47e+01; 0; Mismatches 0; Indels o, Gaps

8

RESULT 11

DO 048311 PRELIMINARY: PRT: 146 AA.

AC Q48381 PRELIMINARY: PRT: 146 AA.

AC Q48381 PRELIMINARY: PRT: 146 AA.

D7 01-NOV-1996 (TRENDLEEL. 01, CREATED)

D7 01-NOV-1996 (TRENDLEEL. 07, LAST ANNOTATION UPDATE)

D8 HOAL PROTEIN (FRACHEET).

D8 KLEBSIELLA ARROCATES: SCOTOBACTERIA: FACULTATIVELY ANAEROSIC RODS:

RW 11

D8 CANTENTO: CREATED PROM N.A.

RE 11

RE 27AALM-970;

R

146 ; 16712 MY;

Ouery Match 0.6%; Score 7; DB 2; Length 146; Best Local Similarity 100.0%; Pred. No. 1.47e+01; Matches 7; Conservative 0; Mismatches 0; Indels 6 Gaps

0

S 용 58 LRPSLTG 64 |||||| 372 LRPSLTG 378

RESULT 32

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RESULT 39
REGULT 39
REGULT WAY

TD Q07879, PRELIMINARY; PRT; 167 AA.

CQ 07879, PRELIMINARY; PRT; 167 AA.

CQ 07879, PRELIMINARY; PRT; 167 AA.

CQ 07879, PRELIMINARY; PRT; 167 AA.

PT 01-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)

TO 1-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)

TO 1-NOV-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)

CREMENTED FAME ORF TLUGGAC.

SACCHARONICES CERPTISILE (AMERS TLAST)

CREMENTED, PROM N. A.

RE STATEMENTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

RE SEMETTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.

SQ SEQUENCE 167 AA; 19759 M9; 5AB6F574 CRC12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 0.6%; Score 7; DB 14; Length 149;
Best Local Similarity 100 0%; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                          Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 SRSLPLP 92
|||||||
251 SRSLPLP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103.295 PRELIMINARY; PRT; 149 AA.
082395; PRELIMINARY; PRT; 149 AA.
082395; PRESENTANCEL. O1, CREATED)
01:NOV-1996 (TREMELEEL. O1, LAST SEQUENCE UPDATE)
10:NOV-1996 (TREMELEEL. O6, LAST MANOZATION UPDATE)
10:TUTH-1990 (TREMELEEL. O6, LAST MANOZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        093405;

01.40V-1996 (PREMBLEEL, 01, CREATED)

01.40V-1996 (PREMBLEEL, 01, LAST SEQUENCE TREATE)

01.40V-1996 (PREMBLEEL, 04, LAST ANDERTON UPDATE)

T-CELL LYPSPORDEL VIRUS TYPE 2 REX AND TAX GENES, PARTIAL CDS, CLONE

PAR FX (PRACHENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 LPRLPQR 29
|||||||
401 LPRLPQR 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE-SOMATIC EMBRYOS AT THE STRAIN-DANGER HALF-LONG, TISSUE-SOMATIC EMBRYOS AT THE LIN X., HAMS G.J., EIMCERNAN J.L.;
SUBHITTED (AAH-11996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, U47094; G1176965;
FRAM, FPOODLI, HEPDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 09:28:30 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOURNE FROM N.A.

KEDLINE; 9619054,

KEDLINE; 9619054,

KEDLINERA N. POYOA P., HONKEN C., OLIVIERA H.D., OLIVIERA O.D., ISHAK R.,

GLIVIERA N. P., LAUREIRO P., ISHAK M., ACEVEDO V., HANGESHIAK N.,

EUS S.W., KUBO T., HALL W.W.,

J. VIROL, 70:1401-1492(1995),

ENGLIEUT 10:1401-1492(1995).

ENGLIEUT 10:1401-1492(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMAN T-CELL LYMPKOTROPIC VIRUS TYPE II.
VIRIDAE: SS-RAN NOKENVELOPED VIRUSES; POSITIVE STRAND RNA VIRUSES;
RETROVIRIDAE; NOKOVIRINAE, TYPE C ONCOVIRUS GROUP;
HAMMALIAN TYPE C ONCOVIRUSES.
                                                                                                                                                                                                                                                                                    SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; E73147; E245470; .
SEQUENCE 167 AA; 19759 MW; SABBF574 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 153 AA; 18394 MW; A7D65CA5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-ROY-1996 (TREMELREL. 01, CREATED)
01-NOY-1996 (TREMELREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1996 (TREMELREL. 07, LAST ANOTATION UPDATE)
18-AT-SHOCK COCKATE (FRAGMENT).
DAUGUS CAROTA (CARROT).
DAUGUS CAROTA (CARROT).
EMBRITONIC CAROTA; PLANTA; EMBRIOPHITA; ANGIOSPERMAE; DICOTTLEDONEAE; APTALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEMAN T-CELL LYAPHOTROPIC VIRUS TYPE II.
VIRIDAE: 55-RNA NONENVELOPED VIRUSES: POSITIVE STRAND RNA VIRUSES:
RETROVIRIDAE: GROCOVIRINAE: TYPE C ONCOVIRUS GROUP;
RAMANIAN TYPE C ONCOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESDOURKE FROM N.A.
STRAIN-SPI PY.
EZRAKU N. NOVAR P., NONKEN C., OLIVIERA M.D., OLIVIERA O.D., ISHAK R.,
DIJVIERA M.P., LAUREIRO P., ISHAK M., ACEVEDO V., HAMMERSHIAK N.,
ERU S.W., KUBO T., ISALK M., M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBELLIFERAE.
                     36 DGLLLRL 42
                                                                                                          Score 7; DB 3; Length 167; Pred. No. 1.47e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 10; Len
Pred. No. 1.47e+01;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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ID Q39680
AC Q39680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dec 21 09:28:30 1991
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100 0%; Pred. No. 1.47+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 10.08; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107.4.41 PRELIMINARY; PRT: 170 AA.
073454 PRELIMINARY; PRT: 170 AA.
073454; OTREMELEEL. 07, CREATED)
01-MG-1999 (TREMELEEL. 07, LAST SEQUENCE UPDATE)
01-MG-1999 (TREMELEEL. 07, LAST ANNOTATION UPDATE)
01-MG-1999 (TREMELEEL. 07, LAST ANNOTATION UPDATE)
REX PROTEIN.
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TISSIDEMENTS CORD:
TISSIDEMENTS CORD:
REDILIES, 97197868.
BRUIS D. EMERS S. YANG C., OSSIG R., JERONIN A., JARN
BRUIS D. EMERS S. TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S. TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
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BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
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BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
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BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUIS D., EMERS S., TANG C., OSSIG R., JERONIN A., JARN
BRUS D., JARN
BRUS D
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1082399 PRELIMINARY: PRT: 149 M.
1082399: 101-WOV-1996 (TREMBLEEL: 01. CREATED)
101-WOV-1996 (TREMBLEEL: 02. LAST SECUENCE UPDATE)
101-WOV-1996 (TREMBLEEL: 05. LAST SECUENCE UPDATE)
101-WOW-1996 (TREMBLEEL: 05. LAST SECUENCE UPDATE)
101-WOW-1996 (TREMBLEEL: 05. LAST SECUENCE UPDATE)
101-WOW-100 1 PX (FRAGMENT).
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EMBL: UZ2873; G1463041; -.
NON TER 1
1 7564 MM; 7BIAD4AC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GLPAPGA 20
|||||||
237 GLPAPGA 243
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251 SRSLPLP 257
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STOLINEMAKING I (MAXI) PX:
STOLINEMAKING I (MAXI) PX:
STOLINEMAKING I (MAXI) PX:
STOLINEMAKING PX:
STO
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VIRIDAE; SS-RUA NONEWVELOPED VIRUSES; POSITIVE STRAND
RETROVIRIDAE; ONCOVIENUE, TIPE C ONCOVIENUS GROUP;
MANDALIAN TIPE C ONCOVIENUEES.
SEQUENCE FROM N.A.
LETOGRAFUR F.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2B.
VIRUSES: RETROLID VIRUSES; RETROVIRIDAE; BLV-HTLV RETROVIRUSES;
HUMAN T-CELL LYMPHOTROPIC VIRUS TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            882 DGLLLRL 888
                                                                                                                                                                                                      EQUENCE PROM N.A.
ETORREUER F., D'AURIOL L., DAZZA M.C., PETEERS M., BEDJABAGA I.,
IOT P., DELADARTE E., GESSAIN A., MONFLAISIR N.,
CEN. VIROL. 79:269-277(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 5; Length 169;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
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ID 055835; PRELIMINARY:
AC 056835; PRELIMINARY:
AC 056
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      Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100,0%; Pred. No. 1.47e+0];
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100 0%; Pred. No. 1.47e+01;
Matches 7; Conservative 0; Mismatches 0; Indels
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O85501 PRELIMINARY; PRT: 170 AA.
085501, PRESIMEEL. 01. CREATED)
01.80V-1996 (TREMBLEEL. 01. AST EXCURNIC UTDATE)
01.80V-1996 (TREMBLEEL. 01. AST EXCURNIC UTDATE)
01.80V-1996 (TREMBLEEL. 01. AST EXCURNIC UTDATE)
01.80V-1996 (TREMBLEEL. 01. AST TANOTATION UTDATE)
01.80V-1996 (TREMBLEEL. 01. AST TANOTATION UTDATE)
1181AN I "-CELL HUMPHOTROPIC VIEWS TIPM VIEWERS, POSITIVE STRAND RNA
METROVIELLARE. ONCOVIENSES. TO CONCOVIENUS GROUP;
111ANDALIAN TIPE C ONCOVIENUSES.
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251 SRSLPLP 257
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SEQUENCE 170 AA; 18402 MW; BCE45442 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 GSILSTL 68
||||||||
856 GSILSTL 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOSEMBLATY J.;
SUBMITTED (NOY-1966) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL, M10060: G319560;
SEQUENCE 170 AA; 18463 MW; 00011EB2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 182 AA; 21000 MW; ADB431D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEOCIEMCE FROM H.A.
STRAINHAIM;
HU P., ELLIOYT J., MCCREADY P., SKOWRONSKI E., GARNES J.,
KOSAKASHI A., CARRANO A.V., BRUDAKZER R., GARCIA E.;
KOSAKASHI A., CARRANO A.V., BELGAKZER BARKJODSJ DAYA BARKS.
SUBHITTED (MAR. 1998) TO SELG/GENBANK/DDSJ DAYA BARKS.
EUSL; APOS3946; G2996260; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERSINIA PESTIS.
PLASKID PODI.
PROKANTOYA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ENDIREC REGM M.A.
ENDIRE: 95186274.
TOLMSTROM A. ROSQVIST R., WOLF-MATZ R., FORSBERG A.;
REPOT. IMMUM. 63:2269-2276(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEMOZEKCE FROM N.A.
SEMOZEKCE FROM N., GOLDE D.R.,
DEEN I.S., MIRA, M., SUGIMURA T., GOJOBORI T., GOLDE D.R.,
PROC. INTL. ACAD. SSI. U.S.A. 02:3101-3105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEOURNCE PROM N.A.
HEDLINE: 64250.199
NODROSKI J., PATANCA R., PERKINS D., BRIGGS D., LEE T.H., ESSEX H.
COLLGAN, J., MONG-STAAL F., GALLO R.C., MASELTINE W.A.;
SCIENCE 23:411-424(1994).
                                                                                                                                                                                                                                                   BÖUENCE FROM N.A.
IOLNSTRYM A.M.;
IOBNITIED (DEC.1994) TO ENBL/GENBANK/DDBJ DATA BANKS
IOBNITIED (DEC.1994); -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rsinia pseudotuberculosis.
Askid piel.
Okaroya, gracilicutes, scotobacteria; pacultatively anaerobic rods;
Terobacteriaceae.
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                                                                                                                                                                           182 AA; 20999 MW; C744A6FD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , CREATED)
, LAST SEQ!
, LAST ANN
Score 7; DB 2; Length 182;
Pred. No. 1.47e+O1;
O; Mismatches O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 2; Length 182;
Pred. No. 1.47e+01;
0; Mismatches 0; Indels
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ANNOTATION UPDATE)
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Gaps
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10 65114 PRELIMINAT; PR

10 65114 PRELIMINAT; PR

10 1.40V-196 (TREMBLEEL 01, L881

10 1.40V-196 (TREMBLEEL 01, LA87

10 1.40V-196 
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RESULT 47

ID 971395;
AC 971395;

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ID 068704

AC 068704;

DT 01-AUG-1998 (
DT 01-AUG-1998 (
DT 01-AUG-1998 (
DE YOPK (YOPQ)

GN YOPK/YOPQ.
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Best Local Similarity 100.0%;
Matches 7; Conservative
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Best Local Similarity 100.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1116 GSLRTAQ 1122
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NAKAYMAK K.I., TOKITO S., NAKAUCHI H., GACHELIN G.;

LIMDINGGENETICS 0:0-0(0).

EMCLI. D90146: E38881: -.

FRAM: PFO0129, NMC_I.

SEQUENCE 184 AA; 21191 MM; 8545770D CRC32;
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|||||||
251 SRSLPLP 257
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REDLINER, 953506.30

REDLINER, 
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VIRIDAE: SS-RNA ENVELOPED VIRUSES; POSITIVE-STRAND; RETROVIRIDAE;
OKCOVIRINAE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECURNCE FROM N.A.
KEDLINE: 9332307.
NARDI D., SWITZER W.M., HADLOCK K.G., KAPLAN J.E., LAL R.B.,
POLES T.M.
7. VIROL. 67:4659-4664(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 SRSLPLP 113
|||||||
251 SRSLPLP 257
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|||||||
| 856 GSILSTL 862
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B (TREMBLREL. 07,
B (TREMBLREL. 07,
) HOMOLOG (YOPQ).
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Pred. No. 1.47e+01;
0; Mismatches 0; Indels
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Pred. No. 1.47e+01;
0; Mismatches 0;
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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RESULT 49

RESULT 49

DO 0.188500

DO 0.1885109 (TRESULEZI. 0). CREATED)

DO 0.18851998 (TRESULEZI. 05. LATT SEQUENCE UPDATE)

RE SEQUENCE FROM N.A.

RESULT 1. SUPERIN R. FAVELLO A. PULTON L. CARDNER N. BOWIELD J.

RE SEQUENCE FROM N.A.

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RESULT 1. SUPERIN R. FAVELLO A. PULTON L. CARDNER N. RESULT N.

RE SEQUENCE FROM N.A.

RESULT 1. SUPERIN R. FAVELLO A. PULTON L. CARDNER N. RESULT N.

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RESULT 1. SUPERIN R. RESULT N. COOPER N.

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PROMERICA PROM N.A.

A WILSON R. AINSCOUGH R. ANDERSON K. BANNES C., BERKS M., BONFIELD J.,

A WILSON R. AINSCOUGH R., ANDERSON K., BANNES C., CRANTON M.,

A BURTON J. CONNELL M., COPERT T., COOPER J., COULSON A., CRANTON M.,

A BURTON J. CLISTER N. PAVELLO A., PULTON L., GARDHER A., GREEN P.,

A KINSTEN J. LAISTER N., AATRELLIE P., DONRSON J., KERSHAW J.,

ACTORNAM A., MORTINGE B., O'CALLIGADN M., PRASONS J., BERCT C.,

A KINDRAM A., MORTINGE B., O'CALLIGAN M., PRASONS J., BERCT C.,

A KINDRAM R., SANDERSO D., SHOMMREN R., SANLDON M., SHIH A.,

ANDERSONS J., PROMA S., WALTESTON R., WATSON A., WEINSTOCK L.,

ANDER M. SERGAL J., WHILDMAN P.,

MOTHETICAL PROTEIN

M. WORLE AND SERGAL S., WHILDMAN P.,

M. WORLTON D., WORLDAN P.,

M. WORLTON D., WATSON A., WEINSTOCK L.,

M. WORLTON D., WORLDAN P.,

M. WOLTEN D., WORLDAN P.,

M. WORLTON D., WATSON A., WEINSTOCK L.,

M. WOLTEN D., WORLDAN P.,

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M. WOLTEN D., WORLDAN P.,

M. WOLTEN D.,

M. W
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Matches 7; Conservative
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Best Local Similarity 100,0%; Pred. No. 1.47e+0;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 7; DB 5; Length 206; Best Local Smilarity 100.0%; Pred. No. 1.47e-01; Natches 7; Conservative 0; Mismatches 0; Indels
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NEMBRANE PROTEIN.
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735 VIGAYDT 741
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904 TFLRTLY 910
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WHITE O., CLAYON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;
SCHMITTEED (SEP-1996) O EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. U1384; 1515455; - 43A5EB6A CRC12;
SECUENCE 192 AA; 20590 NH; 43A5EB6A CRC12;
                                                                                                                                                                            135 LFDVFLR 141
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|827 LFDVFLR 833
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STRAIN=168;
SADAIE Y., YATA K., FUJITA M., SAGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRILLIPS CA. SPRIGGS T. HEDRICH E. COTTON H.D. UTTEBBACK T.R.,
BANNA H.C., KOUTER D.T., SADDER D.M., BRANDON R.C., FIRE L.D.,
PRITCHEMAN J.L., PRANCE C.M., SMITH H.O., VENTEN C.L.,
MCDONALD L.A., SMALL K.V., FRASEN C.M., SMITH H.O., VENTEN J.C.,
SCIENCE 309-486-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQUENCE PROM N.A.
TATUSUV R., MUSHEGIAN A.R., BORK P., BROWN N.P., BAYES W.S.,
ORDODOSKY M., KUDD K.E., KOONIN E.V.;
THER. BIOL. 6:279-291(1996).
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ROKARYOTA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OUDSMCE PROM N.A.

EIGECHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,

EIGECHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KERAICK J.M.,

RILANGE A.R., BULT C.J., TOMB J.F., DOUGHERT B.A., MERRICK J.M.,

TOTTEN R., SUTTON G., FITTHIGH W., FIELDS C.A., GOCKNES J.D.,

TILLIPS C.A., SPRIGGS T., HEDBLOM E., COTYON M.D., UTTERBACK T.R.,

NUNA M.C., KOUTEN D.T., SADDEK D.M., BRANDON R.C., FIRE L.D.,

NUNA M.C., KOUTEN D.T., SADDEK D.M., BRANDON R.C., FIRE L.D.,

TOMBALD L.A., SHALLE N.Y., FRASER C.M., SHITH M.O., VENTER J.C.,

TOMBALD L.A., SHALLE N.Y., FRASER C.M., SHITH M.O., VENTER J.C.,

THENTIED (JUL-1995) TO EMBL/CENBANK, DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1996
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              822
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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0; Mismatches 0; Indels
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AA.
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RE STUDIES FROM N.A.

RE STRAIN-168:

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STRAIN-161
STRAIN-167
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UBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAIE Y., YATA K., FUJITA M., SÁGAI H. .
ASAWARA N.;
BMITTED (APR-1997) TO EMBL/GENBANK/DDDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 7; DB 2; Length 205
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US-08-951-733-20.rept
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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,

A BURNEN S., CONNELL M., COPSET T., COOPER J., COLLOIN A., CHANDEN M.,

A DEAR S., DU E., DORBIN R., FAVELLO A., FULTON L., CARDIER M., CREEN P.,

A ANAKINS T. HILLEE M., JER M., DORBSTON L., ONDES M., KERSIAN J.,

A KIRSTEN J., LAISTER N., LATRELLE P., LICHTNING J., LLOTD C.,

UN KITHER M., MONTINGES B., O'CALLAGHAN M., PARSONS J., DERCT C.,

UN RITHER L., ROOPEN A., SANDERS D., SHONMEZEN R., SMALDON N., SMITH A.,

AN SONINAMEER E., STALEE R., SULTAN J., THERMY-THEE J., THOMAS K.,

A VALDIEN K., VACULNA K., RATESSTON R., WATSON A., WEINSTOCK L.,

RA VALDIEN SEROAT J., WOLLMAN P.,

RA WALTER J 68: 121-18(1994).

DR EDGL: ES145E E189711. Query Match 0.68; Score 7; DB 5; Length 209; Best Local Similarity 100.01; Pred. No. 1478+01; Matches 7; Conservative 0; Mismatches 0; Indels NOM_TER 1 1 SEQUENCE 209 AA; 24388 MW; 80CFFAA2 CRC32; -CAN-1998 (TREMBLEEL. OS, CREATED)
-CAN-1998 (TREMBLEEL. OS, LAST SEQUENCE UPDATE)
-CAN-1998 (TREMBLEEL. OS, LAST ANNOTATION UPDATE)
7010 3 (TRAGEST)
-CAN-1998 (TREADLEEL. OS, LAST ANNOTATION UPDATE)
1010 3 (TRAGEST)
-CAN-1998 (TREADLEEL)
-CAN-1998 (TREADLEEL, OS, LAST ANNOTATION TRACE)
-CAN-1998 (TREADLEEL, OS, LAST ANNOTATION TRACE, CONTRACE)
-CAN-1998 (TREADLEEL, OS, LAST ANNOTATION TRACE, CONTRACE,
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